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;
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
;
US-08-867-087B-10

Query Match      10.6%; Score 92.2; DB 2; Length 945;
Best Local Similarity 67.4%; Pred. No. 1.1e-16;
Matches 130; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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QY 181 TCAACTACGCTGA 193
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RESULT 9
US-08-592-214A-7
; Sequence 7, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..968
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1345
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; OTHER INFORMATION: /note= "product = Zea mays AP1"
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US-08-592-214A-7

Query Match      10.6%; Score 92; DB 1; Length 1345;
Best Local Similarity 48.5%; Pred. No. 1.6e-16;
Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTCAACAGGCGAGGTGACC 60
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Db 209 TTCTCCAAAGCGCGGAAACGGGCTGCTCAAGAGGCGCACGAGATCTCCGTCTCTCTCGCAT 268
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Db 269 GCGGAGGTGCGGCTCATGCTCTCTCCCAAGGCGAAGCTTACGAGTACGCCACCGAC 328
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QY 409 GACAAAGCAGTCCAAAGTTCGTGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAG 468
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QY 589 CAGATA 594
Db 749 CAGACA 754

RESULT 10
US-08-659-188-7
; Sequence 7, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
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/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/659,188
/ FILING DATE: 05-JUN-1996
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-UD 1946
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1345 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 149..968
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1..1345
/ OTHER INFORMATION: /note= "product = Zea mays AP1."
/ US-08-659-188-7

Query Match 10.6%; Score 92; DB 3; Length 1345;
Best Local Similarity 48.5%; Pred. No. 1.6e-16;
Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGCGAGGTGACC 60
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QY 61 TACTCCAAAGAGGAGGAATGGGATTATCAAGAAGCAAGAGATCACTGTTCTATGTAT 120
DB 209 TTCTCCAAAGCGCGGAGGAGGCTGCTCAAGAAGCGCGAGAGATCTCCGTCCTCTCGAT 268
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DB 449 AAAAAATTGAGACCAATACAAAATGCAACAGCACCTGATGGGAGAGATCTAGAGTCTTTG 508
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QY 469 AATAGCGCTCTACTTATAGCTGCAAAAACACAGAGGATGAATAAAGAGATGTG 528
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US-08-655-227-7
RESULT 11
US-08-655-227-7
/ Sequence 7, Application US/08655227
/ Patent No. 6025483
/ GENERAL INFORMATION:
/ APPLICANT: Yanofsky, Martin P.
/ TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
/ TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/655,227
/ FILING DATE: 05-JUN-1996
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-UD 2143
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1345 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 149..968
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1..1345
/ OTHER INFORMATION: /note= "product = Zea mays AP1."
/ US-08-655-227-7

Query Match 10.6%; Score 92; DB 3; Length 1345;
Best Local Similarity 48.5%; Pred. No. 1.6e-16;
Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGCGAGGTGACC 60
DB 149 ATGGGCGCGGAGGTACAGTCAAGCGATAGAGACAAAGATAAACCGGAGGTGACC 208
QY 61 TACTCCAAAGAGGAGGAATGGGATTATCAAGAAGCAAGAGATCACTGTTCTATGTAT 120
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DB 269 GCCGAGTTCGGCTCATCGTCTTCTCCCAAGGCGAGCTCTACAGTACGCCACCGAC 328
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QY 589 CAGATA 594
Db 749 CAGACA 754

RESULT 12

US-08-655-241-7
; Sequence 7, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yancofsky, Martin F.
; APPLICANT: Weigel, Detlef
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,241
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: CLASS 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Kathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..968
FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays AP1."
US-08-655-241-7

Query Match 10.6%; Score 92; DB 3; Length 1345;
Best Local Similarity 48.5%; Pred. No. 1.6e-16;
Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

QY 1 ATGGGACCTGGGAAGCTTGGAGATCAAGAGGATTTGAGAACTCAAGTAACAGCAGGTGACC 60
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Db 629 CTGAGGAGGAGACAAGGCTCTGCAAGAGGAACTTGGCGAGGCGCAGAAAGGCCGCTCGG 688
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Db 749 CAGACA 754

RESULT 13

US-09-149-976-7
; Sequence 7, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yancofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States

Db 209 TTCTCCAGCGCGGAAAGCGCTGCTCAAGAGGCGCAGAGATCTCCGTCCTCTCGCAT 268
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QY 181 TCAACTACGCTGACAGAAATCTTGGCAA-----ATACCATGGACAATCTGGG 228
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QY 229 AAGAAGTTGGGATGCTAAGCATGAGAACTCAGCAATGAAGTGGATAGAGTCAAGAAA 288
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Db 749 CAGACA 754

RESULT 15

US-08-904-284-2
; Sequence 2, Application US/08904284
; Patent No. 6133435
; GENERAL INFORMATION:
; APPLICANT: Fernandez, Donna E.
; APPLICANT: Heck, Gregory R.
; TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,284
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.94193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-904-284-2
Query Match 10.5%; Score 91; DB 3; Length 795;
Best Local Similarity 66.7%; Pred. No. 2.3e-16;
Matches 130; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
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Job time : 77.5395 secs

GenCore version 5.1.6
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(without alignments)
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Title: US-10-069-527-1

Perfect score: 868

Sequence: 1 atgggacgtgggaagtgtga.....aaaaaaaaaaaaaaaaaaaaa 868

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	259	29.8	780	6 ABK82086	Abk82086 Novel flo
6	259	29.8	783	6 ABK82087	Abk82087 Novel flo
7	288.4	29.8	1065	6 ABK82124	Abk82124 DNA encod
8	257.4	29.7	764	6 ABK82089	Abk82089 Novel flo
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10	256.8	29.6	789	6 ABK82085	Abk82085 DNA encod
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17	148.2	17.1	681	4 AAF85393	Aaf85393 Nucleotid
18	148.2	17.1	946	4 AAF85392	Aaf85392 Nucleotid
19	148.2	17.1	946	6 ABK88485	Abk88485 Poplar pr
20	148.2	17.1	946	8 ACA62518	Aca62518 Poplar ho
21	147.4	17.0	882	2 AAC51189	Aac51189 Homeotic
22	146.6	16.9	924	3 AAZ57943	Aaz57943 Poplar fl
23	138.8	16.0	446	3 AAC48151	Aac48151 Zea mays

24	136.2	15.7	982	4 AAS00104	Aas00104 Granny Sm
25	133.8	15.4	926	6 AAD42259	Aad42259 Soybean A
26	130.4	15.0	1257	6 AAD42257	Aad42257 Corn AP3
27	128.4	14.8	989	3 AAC55879	Aac55879 Eucalyptu
28	124.2	14.3	959	3 AAC40831	Aac40831 Arabidops
29	122.6	14.1	954	3 AAC51525	Aac51525 Arabidops
30	122.6	14.1	1170	3 AAC51790	Aac51790 Arabidops
31	122	14.1	495	3 AAC48125	Aac48125 Zea mays
32	121.8	14.0	954	3 AAC40685	Aac40685 Arabidops
33	119.4	13.8	121	6 ABK25454	Abk25454 Male-ster
34	119.4	13.8	121	6 ABK25462	Abk25462 Male-ster
35	119.4	13.8	121	6 ABK25466	Abk25466 Male-ster
36	119.4	13.8	121	6 ABK25458	Abk25458 Male-ster
37	119.4	13.8	121	6 ABK25453	Abk25453 Male-ster
38	119.4	13.8	121	6 ABK25465	Abk25465 Male-ster
39	119.4	13.8	121	6 ABK25461	Abk25461 Male-ster
40	119.4	13.8	121	6 ABK25457	Abk25457 Male-ster
41	112	12.9	386	3 AAC57268	Aac57268 Eucalyptu
42	109.8	12.6	613	3 AAC57279	Aac57279 Eucalyptu
43	109	12.6	909	3 AAF85364	Aaf85364 Plant Fra
44	109	12.6	4285	4 AAF85391	Aaf85391 Nucleotid
45	109	12.6	4285	6 ABK88484	Abk88484 Poplar pr

ALIGNMENTS

RESULT 1
AAS00103
ID AAS00103 standard; cDNA; 868 BP.
XX AC AAS00103;
XX 11-SEP-2003 (revised)
DT 17-MAY-2001 (first entry)
XX DE Granny Smith apple cDNA encoding MdPI.
XX KW Granny Smith apple; MdPI; seedless fruit; horticulture;
KW accelerated breeding programme; cross pollination; transgenic plant;
KW biennial bearing tendency; codling moth; ss.
XX OS Malus x domestica; var. Granny Smith.
XX FH Key Location/Qualifiers
FT CDS 1..848
FT /tag= a
FT /product= "MdPI"
FT primer_bind 1..15
FT /tag= b
FT /label= PCR_primer_P1_binding_site
FT primer_bind 19..41
FT /tag= c
FT /label= PCR_primer_P5_binding_site
FT primer_bind 291..312
FT /tag= d
FT /label= PCR_primer_P3_binding_site
FT primer_bind 314..334
FT /tag= e
FT /label= PCR_primer_P4_binding_site
FT primer_bind complement(609..626)
FT /tag= f
FT /label= PCR_primer_P2_binding_site
FT primer_bind complement(770..791)
FT /tag= g
FT /label= PCR_primer_P7_binding_site
FT primer_bind complement(818..840)
FT /tag= h
FT /label= PCR_primer_P6_binding_site
XX WC200117334-A1.
XX 15-MAR-2001.

DR WPI; 1994-026218/03.
DR P-PSDB; AAR46555.
XX New nucleic acid which alters flower morphology - by suppressing petals
PT and stamen(s), or converts them to other organs, partic. to produce
PT transgenic plants less susceptible to insect pests.
XX
PS Disclosure; Fig 1A; 33pp; English.
XX
XX A flower specific gene fbpl was isolated from the genome of Petunia
CC hybrida. This gene has the features of a transcription factor and belongs
CC to the group of MADS box genes. The fbpl gene is only active during
CC differentiation of floral organ primordia and plays a crucial role in the
CC determination of part of the floral meristem into petals and stamen.
CC primordia. Plants transformed with the gene are less attractive to insect
CC pests so have better resistance to them; specifically cucumber plants are
CC protected against Frankliniella occidentalis but the method can be used
CC for other, esp. parthenocarpic and/or apomictic plants. The plants are
CC also less susceptible to secondary fungal infection. Elimination of
CC petals may improve photosynthesis and seed yield may be increased. See
CC also AAQ55090-3. (Updated on 05-MAR-2003 to correct PN field.) (Updated
CC on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 780 BP; 277 A; 120 C; 172 G; 211 T; 0 U; 0 Other;
XX
XX Query Match 33.6%; Score 291.4; DB 2; Length 780;
XX Best Local Similarity 67.8%; Pred. No. 7.5e-64;
XX Matches 444; Conservative 0; Mismatches 196; Indels 15; Gaps 2;
XX
QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACGCGAGGTGACC 60
DB 8 ATGGGAGAGGAGGATAGATAGATAAAGAAAGTAAAGAACTCAAGCAACGACAGTAACT 67
QY 61 TACTCCAGAGGAGGAGGATGAGTATCAAGAGGCAAGGAGATCACTTCTTATGTGAT 120
DB 68 TACTCAAAAAGAGAAATGGGATCTTGAAAAAGCTTAAGGAAATAGTGTCTTTGTGAT 127
QY 121 GCTAAAGTATCTTATCAATTTATCTAGCTCTGGGAAGATGTTGTAATCTCAGCCCT 180
DB 128 GCTCGTGTCTGTATCAATTTTGTAGCTCTGGCAAGATGATGATGTTCT-----CT 181
QY 181 TCAACTACGCTGACAGAAATCTTGCAAAATACCATGGCAATCTGGGAAGAAGTTGTGG 240
DB 182 TCTACTTCGTTGTTGATATTTTGGATCAATATCACAAGCTTACTGTGTAAGATTGTTG 241
QY 241 GATCTAAGCATAGAGACCTCAGCAATGAAGTGGATAGTCAAGAAAGCAATGACAGC 300
DB 242 GATCTAAGCATAGAGACCTTGGCAATGAATCAAAAGTCAAGAAAGCAATGACAC 301
QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCATCAATTAACCATGTAGAG 360
DB 302 ATGCAAAATGAACCTCAGGCATCTGAAGGTTGAAGATATCATCTTTGAACCATAGAG 361
QY 361 CTGATGCCCTTAGAGGAGCACTTGAATGGCCTTCAAGTATCCGGGACAGCAGTCC 420
DB 362 CTCATGATATTTGGGAAGATGCCCTTGAATGGACTCTACTAGTATTCGTAACAACAGAA 421
QY 421 AAGTTTCGTCGATGATGAGAGCAATGGAAGGCACTTGAAGATGAGAAATAGAGCGCTC 480
DB 422 GAGTTCTGAGATGATGAGAAAGAAAGACTCAAGTATGGAGGAGGAGCAAGCACTT 481
QY 481 ACTTATGAGCTGCAAAAACAACAGGAGATGAAATATAAGAGATGTGAGAAACATGGAA 540
DB 482 AATTGCCAATTTGGCCCACTTGGATAGCAACCATGAATAGGAATATGGGAGAAATGGC 541
QY 541 AATGGGTATCATCAGAGCAGCTGGGAACTTACCAACCAACACAGCAGCAGATACCTTTT 600
DB 542 GAAGTGTTCAGCAGAGGGAG-----AATCATGCTACCAAAACCATATGCCCTTT 592
QY 601 GCCTTCGCGTCGAGCCTTATTCAGCAAAATCTCCAGGAGAGAAATCTAATTAGATA 655
DB 593 GCCTTCGAGTACACCAACCAATGACGCAAAATTTGAGGAGAGGTTGTAATAAAGAA 647

RESULT 3
ADD55880
ID ADD55880 standard; cDNA; 896 BP.
XX
AC ADD55880;
XX
DT 15-JAN-2004 (first entry)
DE Thalecress environmental stress-related cDNA #127.
XX
KW Thalecress; environmental stress; ss; plant; viral infection;
KW fungal infection; microbial infection; herbicide resistance; heat; cold;
KW heavy metal; low light; drought; osmotic stress; salt concentration;
KW transgenic.
XX
OS Arabidopsis thaliana.
XX
PN US2003131386-A1.
XX
PD 10-JUL-2003.
XX
PF 22-OCT-2002; 2002US-00278536.
XX
PR 23-MAR-1999; 99US-0125814P.
XX
PR 22-MAR-2000; 2000US-00532591.
XX
PA (SANA/) SAMAHA R.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (KEDD/) KEDDIE J.
PA (RATC/) RATCLIFFE O.
PA (PILG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (ZHAN/) ZHANG J.
XX
PI Samaha R, Heard J, Jiang C, Pineda O, Reuber L, Riechmann JL;
PI Yu G, Keddie J, Ratcliffe O, Pilgrim M, Adam L, Broun P, Zhang J;
XX
DR WPI; 2003-829608/77.
XX
XX New recombinant polynucleotide for altering the regulation of gene
PT expression of plants to modify the plant's traits, particularly the
PT plant's environmental stress tolerance.
XX
XX Claim 14; SEQ ID NO 238; 219pp; English.
XX
CC The invention relates to a recombinant polynucleotide that alters a
CC plant's environmental stress tolerance when compared with the same trait
CC of another plant lacking the recombinant polynucleotide. Also included
CC are a transgenic plant comprising the novel recombinant polynucleotide
CC having a sequence that encodes a polypeptide comprising at least 6
CC consecutive amino acids of any of the 55 250-500 residue amino acid
CC sequences (s1), given in the specification, altering the environmental
CC stress response or tolerance of a plant, or altering a plant's trait and
CC altering the expression levels of at least one gene in a plant. The
CC recombinant polynucleotide and methods are useful for altering the
CC regulation of gene expression of plants to modify the plant's traits, in
CC particular with respect to environmental stress responses (e.g. to viral
CC infection, fungal infection, microbial infection, herbicide resistance,
CC heat, cold, heavy metals, low light, drought, osmotic stress and salt
CC concentration). The present sequence is an environmental stress related
CC polynucleotide of the invention.
XX
SQ Sequence 896 BP; 285 A; 143 C; 218 G; 250 T; 0 U; 0 Other;

Query Match 30.6%; Score 265.2; DB 9; Length 896;
Best Local Similarity 68.0%; Pred. No. 3.6e-57;

RESULT 5

ABK82086
 ID ABK82086 standard; cDNA; 780 BP.
 XX
 AC ABK82086;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 XX Novel floral meristem identity gene LpMADS1 contig #1.
 XX
 DE Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 XX CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 XX HB-like protein; plant growth; plant architecture;
 XX inflorescence development; flower development; embryo development;
 XX seed development; flower organ identity; phase change; male sterility;
 XX hybrid seed production; herbage quality; early maturing crop;
 XX biomass increase; branching increase; blocking flowering;
 XX allergenic pollen; floral meristem identity protein; ss.
 XX
 OS Lolium perenne.
 XX
 FN WO200233091-A1.
 XX
 PD 25-APR-2002.
 XX
 XX 17-OCT-2001; 2001MO-AU001311.
 XX
 XX 19-OCT-2000; 2000AU-00000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX
 PA (AGRE-) AGRESEARCH LTD.
 XX
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-454601/48.
 XX
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 XX CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 XX fescue species, useful for controlling plant life cycles and/or growth
 XX phases.
 XX
 XX Claim 3; Fig 29; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles

SQ Sequence 780 BP; 229 A; 203 C; 206 G; 136 T; 0 U; 6 Other;
 Query Match 29.8%; Score 259; DB 6; Length 780;
 Best Local Similarity 64.5%; Pred. No. 1.3e-55;
 Matches 426; Conservative 0; Mismatches 216; Indels 18; Gaps 2;
 QY 1 ATGGGACGTGGGAGTTGAGATCAAGAGGATGAGAACTCAAGTAACAGCAGGTGACC 60
 DB |||||
 QY 84 ATGGGCGGTGGGAAGATCGAGATCAAGAGGATCGAGAACCAAGCCGAGGTGACC 143
 DB |||||
 QY 61 TACTTCAAGAGAGAGAAATGGGATTTATCAAGAGGCAAGAGAGATCACTTGTCTATGTGAT 120
 DB |||||
 QY 144 TTCTTCAAGCGCAAGACGGGATCTCTCAAGAGGCCAAGAGAGATCAGCGTCTCTGGCAC 203
 DB |||||
 QY 121 GCTAAAGTATCTCTTATCATTTATTTCTAGCTCTGGGAAGATGGTTGAATCTGAGCGCT 180
 DB |||||
 QY 204 GCCGAGGTGGGCTGCTGCTCTTCTCCAGCGCGGCAAGCTCTACGACTTCTGCTCCCA 263
 DB |||||
 QY 181 TCAACTAGCTGACAGAAATCTTGACAAATACCATGGACAACTCTGGGAAGAGTTGTGG 240
 DB |||||
 QY 264 AAGACATCGCTATCAAGATCTTGGAGAGTACCAGACCACTCCGGAGATACTGTGG 323
 DB |||||
 QY 241 GATGCTAAGCATGAGAACCTCAGCAATGAAGTGGATAGAGTCAAGAAAGACAATGACAGC 300
 DB |||||
 QY 324 GATGAGAAACACAAGAGCCTCAGTGGGAGATTGATCGAATCAAGAAAGAAAATGACAAC 383
 DB |||||
 QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 DB |||||
 QY 384 ATGCAGATCGAGCTCAGGCATCTGAAAGGCGGAAGATCTGAACTCCTGCAACCCCAAGAG 443
 DB |||||
 QY 361 CTGATGGCCTTAGAGGAAGCACTTGAATAAGTGGCCTTACAAGTATCCGGGCAAGCAGTCC 420
 DB |||||
 QY 444 TTGATCATGATTGAGGAAGCACTTGAATAGTACTGACAGGCTGCGATGAAACAGATG 503
 DB |||||
 QY 421 AAGTTCGTGCATGATGAGAGACAATGGAAGGCACTGGAAGATGAGATTAAGCGCTC 480
 DB |||||
 QY 504 GAGCACTACGACAGCGCTGATGAAACCTGGCAAGATGCTAGAAGATGAGAACAGTTGCTC 563
 DB |||||
 QY 481 ACTTATGAGCTGCAAAACCAACAGGAGATGAAATAAAGAGAAATGTGAGAAACATGAA 540
 DB |||||
 QY 564 GCATCTAAACTGC---ATCAGCAGATATTGCGCTGAACGGGACATGAGGGAGCTTGAG 620
 DB |||||
 QY 541 AATGGTATCATCAGAGCAGCTGGGAACTACAAACAAACCAAGCAGCAGATACCTTTT 600
 DB |||||
 QY 621 CTGGTTACCATCCG-----GACAGGGACTTTGCGAGCCAGATGCCGATC 665
 DB |||||
 QY 601 GCCTTCGCGTGCAGCCTATTTCAGCCAAATCTCCAGGAGAGAAATCTAATTAGATATATCT 660
 DB |||||
 QY 666 ACGTTCGCGTGCAGCCTAGCCACCCCACTGCGAGGAGACAGCTAGGCGCGNTTATCT 725
 DB |||||

RESULT 6

ABK82087

ID ABK82087 standard; cDNA; 783 BP.

XX

AC ABK82087;

XX

DT 27-AUG-2002 (first entry)

XX

XX Novel floral meristem identity gene LpMADS1 contig #2.

XX

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;

XX CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;

XX HB-like protein; plant growth; plant architecture;

XX inflorescence development; flower development; embryo development;

XX seed development; flower organ identity; phase change; male sterility;

XX hybrid seed production; herbage quality; early maturing crop;

XX biomass increase; branching increase; blocking flowering;

XX allergenic pollen; floral meristem identity protein; ss.

XX

OS Lolium perenne.

XX

XX WO200233091-A1.

XX

XX PD 25-APR-2002.
 XX PF 17-OCT-2001; 2001WO-AU001311.
 XX PR 19-OCT-2000; 2000AU-00000873.
 XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX PA (AGRE-) AGRESEARCH LTD.
 XX PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX DR WPI; 2002-454601/48.
 XX
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 FT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 FT fescue species, useful for controlling plant life cycles and/or growth
 FT phases.
 XX
 XX Claim 3; Fig 29; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (i), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another. Leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles
 XX
 SQ Sequence 783 BP; 233 A; 204 C; 208 G; 136 T; 0 U; 2 Other;

Query Match 29.8%; Score 259; DB 6; Length 783;
 Best Local Similarity 64.5%; Pred. No. 1.3e-55;
 Matches 426; Conservative 0; Mismatches 216; Indels 18; Gaps 2;
 1 ATGGAGCTGGAGGTTGAGATCAAGAGGATTCAGAACTCAAGTACAGCGAGGTGACC 60
 82 ATGGGGCTGGAGATCGAGATCAAGAGTCAAGACCAAGCAACCCAGGTGACC 141
 61 TACTCCAAAGAGGAGATGGATTCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
 142 TTCTCAAGCGCAAGACGGGATCTCAAGAGGCCCAAGGAGATCAGCGTCTCTGGAC 201
 121 GCTAAAGTATCTTATCATTTATTTAGCTCTGGAGATGGTTGATATCTCAGCCCT 180
 202 GCGAGGTGCGGTGCTGCTTCTTCAGCGCCGCGAGCTCTAGACTTCTGTCCTCCCA 261
 181 TCAACTAGCTGACAGAAATCTTGCAAAATPACCATGGCAATCTGGGAAGAAGTTGTGG 240
 262 AAGACATCGCTATCAAGATCTTGAGAGAGTACCAGACCAACTCCGGGAAGATCTGTG 321

QY 241 GATGCTAAGCATGAGAACTCAGCAATGAAGTGGTAGAGTCAAGAAAGCAATGACAGC 300
 DB 322 GATGAGAAACACAGAGCTCAGTCGGGAGATTGATCGAATCAAGAAAGAAATGACAAC 381
 QY 301 ATGCAAGTAGAGCTCAGCATCTGAAGGAGAGGATATCACATCTTGAACCATGTAGAG 360
 DB 382 ATGCAGATCGAGCTCAGGCATCTTGAAGCGGGAAGATCTGAACTCACTGCAACCCAAAGAG 441
 QY 361 CTGATGGCTTAGAGGAAGCACTTGAAATGCGCTTACAAGTATATCCGGGCAAGAGCTCC 420
 DB 442 TTGATCATGATTGAGGAAGCACTTGATTAATGGACTGACAGGCTGATGAAAAACAGATG 501
 QY 421 AAGTTCTGTCGATGATGAGAGCAATGGAAGGCACTTGAAGATGAGATGAAGCCCTC 480
 DB 502 GAGCACTAGCAGAGCTGATGAAACTGCGCAAGATGCTAGAGATGAGAAACAAGTTGCTC 561
 QY 481 ACTTATGAGCTCAAAAACACAGAGATGAAAATAAAAGAGAAATGTGAGAAACATGGA 540
 DB 562 GCATCTAACTGC---ATCAGCAAGATATTGCGCTGAACGGGAACATGAGGAGCTTGAG 618
 QY 541 AATGGGTATCATCAGAGGAGCTGGGAACTATCAACAACAACAGCAGCAGATACCTTT 600
 DB 619 CTTGGTTACCATCCG-----GACAGGGACTTTTGCAGCCAGATGCCGATC 663
 QY 601 GCCTTCCGCTGCGCTTATTCAGCAAACTCTCCAGGAGAGATCTAATTAGATATATCT 660
 DB 664 AGTTCCGCTGCGCTTATTCAGCAAACTCTCCAGGAGAGATCTAATTAGATATATCT 723
 RESULT 7
 ABK82124
 ID ABK82124 standard; cDNA; 1065 BP.
 XX
 AC ABK82124;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE DNA encoding novel floral meristem identity protein LpMADS1b.
 XX
 KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; flower development; embryo development;
 KW inflorescence development; plant architecture;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; gene; ss.
 XX
 OS Lolium perenne.
 XX
 PN WO200233091-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 17-OCT-2001; 2001WO-AU001311.
 XX
 PR 19-OCT-2000; 2000AU-00000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX
 PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX
 DR WPI; 2002-454601/48.
 DR P-PSDB; ABG60942.
 XX
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 PS Claim 3; Fig 59; 290pp; English.

CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles
XX
SQ Sequence 764 BP; 225 A; 202 C; 206 G; 129 T; 0 U; 2 Other;

Query Match 29.7%; Score 257.4; DB 6; Length 764;
Best Local Similarity 64.4%; Pred. No. 3.2e-55;
Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 1 ATGGGACGTGGGAAGTTGAGATCAAGAGGATTCAGAACTCAAGTACAGCGAGGTGACC 60
DB |||||
84 ATGGGCGCGGAAGATCGAGATCAAGAGGATTCAGAACTCAAGTACAGCGAGGTGACC 143
QY 61 TACTCCAGAGGAGGATGGATTATCAAGAGGCAAGAGGATCACTGTCTTATGTGAT 120
DB |||||
144 TTCTCCAGCGCAGAAACGGGATCTCTCAAGAGGCCAGAGGATCGGTCTCTCGGAC 203
QY 121 GCTAAAGTATCTTATCATTTATCTTCTGCTTCTGGGAAGATGGTTGAATCTCCAGCCCT 180
DB |||||
204 GCGAGGTGCGGCTGCTGCTCTCCAGCGCGCAAGCTCTACGACTTCTCTCTCCCC 263
QY 181 TCAACTACGTGACAGAAATCTTGGCAAAATACATGGAATCTGGGAGAGTGTGG 240
DB |||||
264 AAGACATCGGTATCAAGAACTTGGGAAGTACAGACCACTCCGGGAAGATCTGTGG 323
QY 241 GATGCTAAGCATGAGAACTTCAGCAATGAAGTGTAGATCAAGAAAGCAATGACAGC 300
DB |||||
324 GATGAGAAACACAGAGCCTCAGCGGAGATGATCGAATCAAGAAAGAAATGATAAC 383
QY 301 ATGCAAGTACAGCTCAGGATCTGAGCGGAGAGGATATCATCATTTGAACCATGTAGAG 360
DB |||||
384 ATGCAGATCAGCTCAGGCACTTGAAGGCGAAGATCTGAACCTCACTGCAACCCAAAGAG 443
QY 361 CTGATGCGCTTAGAGGAAGCACTTGAATAATGGCTTACAAGTATCCGGGACAAAGCAGTCC 420
DB |||||
444 TTGATCATGATGAGGAGCACTTGATATGAGTACAGCGCTGATGAAACAGATG 503
QY 421 AAGTTCCTGCATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATGAAGCGCTTC 480
DB |||||
504 GAGCACTACGACAGGCTGATGAAACTGGCAAGATGCTAGAAGATGAGAAAGTTGCTC 563
QY 481 ACTATGAGCTGAAACACAGGAGATGAAATGAAGAGATGTGAGAAACATGGA 540
DB |||||
564 GCATTAACATGCG---ATCAGCAAGATATTGGCTGAAACGGGAACATGAGGGAGCTTGAG 620
QY 541 AATGGGTATCATCAGAGGCGAGTGGGAACTACAACAAACACAGCAGCAGATACCTTTT 600
DB |||||
621 CTGTGTTACCATCG-----GACAGGGACTTTGAGCGCCAGATGCGGATC 665
QY 601 GCCTTCGCGTGCAGCTATTCAGCAAAATCTCCAGGAGAGATCTAATTAGATATATCT 660
DB |||||
666 ACGTTCGCGTGCAGCTATTCAGCAAAATCTCCAGGAGAAACAGCTAGGCGGNTTATCT 725

RESULT 9

ABK82088
ID ABR82088 standard; cDNA; 783 BP.

XX
AC ABK82088;

XX
DT 27-AUG-2002 (first entry)

XX Novel floral meristem identity gene LpVADS1 contig #3.

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;

KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
KW HB-like protein; plant growth; plant architecture;
KW inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KW hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;
KW allergenic pollen; floral meristem identity protein; ss.
OS Lolium perenne.
XX
FN WO200233091-A1.
XX
XX
XX 25-APR-2002.
XX 17-OCT-2001; 2001WO-AU001311.
XX 19-OCT-2000; 2000AU-00000873.
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX (AGRE-) AGRERESEARCH LTD.
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX WPI; 2002-454601/48.
XX
XX New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.
XX
XX Claim 3; Fig 29; 290pp; English.
XX
XX The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or down-regulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles
XX
SQ Sequence 783 BP; 232 A; 204 C; 208 G; 138 T; 0 U; 1 Other;

Query Match 29.6%; Score 256.8; DB 6; Length 783;
Best Local Similarity 64.4%; Pred. No. 4.6e-55;
Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 1 ATGGGACGTGGGAAGTTGAGATCAAGAGGATTCAGAACTCAAGTACAGCGAGGTGACC 60
DB |||||
78 ATGGGCGCGGAAGATCGAGATCAAGAGGATTCAGAACTCAAGTACAGCGAGGTGACC 137

QY 61 TACTCCAGAGGAGGAGGATGATTTATCAAGAGGCAAGAGAGATCACTGTTCTTATGTAT 120
 Db 138 TTCTCCAGGCGCAAGACGGGATCTCAAGAGGCGCAAGAGAGATCACTGTTCTTATGTAT 197
 QY 121 GCTAAAGTATCTTATCATTTATCTAGCTCTGGGAGAGTGTGTAATCTGACGCTT 180
 Db 198 GCCAGGTGCGGTGCTGCTTCTTCCAGGCGCGGAGGATCTTACGATCTGCTCTCCCC 257
 QY 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACCATGGAATCTGGGAGAGTGTG 240
 Db 258 AAGACATCGCTATCAAGATCTTGGAGAGTACCAGACCACTCCGCGAGATAGTGTG 317
 QY 241 GATGCTAAGCATGAGACCTCAGCATGAGTGAAGTGAAGTCAAGAAAGCATGACAGC 300
 Db 318 GATGAGAAACACAGAGCCTCAGCGCGGAGATTTGATCGAATCAAGAAAGAAATGATAAC 377
 QY 301 ATGCAAGTACGCTCAGGCTCAGGCTTGAAGGAGAGATATCATCATTTGAACATGTAGAG 360
 Db 378 ATGAGATCGAGCTCAGGCTTGAAGGCGAGATCTGACTCATCTGCAACCCAAAGAG 437
 QY 361 CTGATGCGCTTAGAGGAGCATTGAAATGGGCTTACAGATATCCGGGACACAGAGTCC 420
 Db 438 TTGATCATGATTTGAGGAGCATTGATATGAGTCTGACAGGCTGATGAAAGAAACAGATG 497
 QY 421 AAGTTCTGCTGACATGATGAGAGACATGGAAGGCACTGAGATGAGATTAAGCGCTC 480
 Db 498 GAGCACTACAGAGCTGATGAAATCTGGCAATGCTGAGATGAGAACTGCTGCT 557
 QY 481 ACTTATGAGTGCACAAACACAGGAGATGAAATTAAGAGATATGAGAAACATGGAA 540
 Db 558 GCATTTAACTGC---ATCAGCAAGATATTCGCTGAACCGGAAATGAGGAGCTGAG 614
 QY 541 AATGGGTATCATCAGAGGCTGCGGAGTACAAACACAGCAGCAGATACCTTTT 600
 Db 615 CTGTTTACCATCG-----GACAGGACTTTGCGCCGAGATGCGGATC 659
 QY 601 GCCTTCGCGTGCAGCTTATTCAGCAAAATCTCCAGGAGAGATCTTAATTAGATATATC 660
 Db 660 ACGTTCCGCTGCGAGCTACCCACCCACCTCAGGAGAAACAGTAGCGGTTAATCT 719

RESULT 10

ABK82085
 ID ABK82085 standard; cdna; 789 BP.

XX AC ABK82085;

XX DT 27-AUG-2002 (first entry)

XX DE DNA encoding novel floral meristem identity protein LpMADS1.

XX KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; gene; ss.

XX OS Lolium perenne.

XX PN WO200233091-A1.

XX PD 25-APR-2002.

XX PF 17-OCT-2001; 2001WO-AU001311.

XX PR 19-OCT-2000; 2000AU-00000873.

XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX PA (AGRE-) AGRESEARCH LTD.

XX XX

PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-454601/48.
 DR P-PSDB; ABG60932.
 XX
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 XX Claim 3; Fig 27; 290pp; English.

CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles

XX SQ Sequence 789 BP; 233 A; 207 C; 211 G; 138 T; 0 U; 0 Other;

Query Match 29.6%; Score 256.8; DB 6; Length 789;
 Best Local Similarity 64.4%; Pred. No. 4.6e-55;
 Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 1 ATGGAGCTGGGAAGTGTGATCAAGAGATTTGAGAACTCAAGTACAGCGAGGTGACC 60
 Db 84 ATGGGCGCGGAGATCGAGATCAAGAGATCGAGAACCAAGCAACCGCCAGGTGACC 143
 QY 61 TACTCCAGAGGAGATGGATATCAAGAGCAAGGAGATCACTGTTCTATGTAT 120
 Db 144 TTCTCCAGGCGCAAGACGGGATCTCAAGAGCGCAGGAGATCAGCTGCTCTGGAC 203
 QY 121 GCTAAAGTATCTCTTATCATTTATTTAGCTCTGGGAGAGTGGTGAATACTCAGCCCT 180
 Db 204 GCCAGGTGCGGCTGCTCTTCTCCAGCGCGGCAAGCTTACGACTTCTGCTCCCC 263
 QY 181 TCACTACGCTGACAGAAATCTTGGCAAAATACCATGGACAATCTGGGAGAGTGTGG 240
 Db 264 AAGACATCGCTATCAAGAACTTTGGAGAGTACAGACCAACTCCGGGAGAGTACTGTGG 323
 QY 241 GATGCTAAGCATGAGAACCTCAGCAATGAAGTGGATAGAGTCAAGAAAGCAATGACAGC 300
 Db 324 GATGAGAAACACAGAGCCTCAGCGCGGAGATTTGATCGAATCAAGAAAGAAATGATAAC 383
 QY 301 ATGCAAGTACAGCTCAGGATCTTGAGGAGAGAGATATCACATCATTTGACCATGTAGAG 360
 Db 384 ATGCAAGTACAGCTCAGGCACTTTGAAGGCGGAGATCTGAATCACTGCAACCAAGAG 443

QY 361 CTGATGCGCTTAGAGGAGCATTGAAATGGCCCTTACAGTCTCCGGGACAGCAGTCC 420
 Db |||||
 QY 444 TTGATCATGATTGAGGAGCACTTGATATGGAATGACAGCTGCTGATGAAACAGATG 503
 Db |||||
 QY 421 AAGTTCTCGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATAAGCGCCTC 480
 Db |||||
 QY 504 GAGCACTACGACAGCTGATGAAACTGGCAAGATGCTAGAAGATGAGAACTAGTTGCTC 563
 Db |||||
 QY 481 ACTTATGAGCTGCAAAACACAGGAGATGAAATTAAGAGATGTGAGAAACATGGAA 540
 Db |||||
 QY 564 GCAATTAATGCG---ATGACAGATATTTGGCTGAAACGGGAACATGAGGGAGCTTGAG 620
 Db |||||
 QY 541 AATGGGTATCATCAGAGCAGCTGGGAACTTACAAACACACAGCAGCAGATACCTTTT 600
 Db |||||
 QY 621 CTGTTTACCATCG-----GACAGGGACTTTGACGCCAGATGCGGATC 665
 Db |||||
 QY 601 GCCTTCGGCTGAGCCTTATTCAGCCAAATCTCCAGGAGAGATCTTAATAGATATATCT 660
 Db |||||
 QY 666 ACGTTCCGCTGCGACCTAGCCACCACTGCGAGGAGAACAGCTAGGCGCTTTAATCT 725
 Db |||||

RESULT 11

ABK82123
 ID ABR82123 standard; cDNA; 979 BP.

XX AC ABK82123;

XX XX 27-AUG-2002 (first entry)

XX DE DNA encoding novel floral meristem identity protein LpMADS1.

XX KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW KW HB-like protein; plant growth; plant architecture;
 KW KW inflorescence development; flower development; embryo development;
 KW KW seed development; flower organ identity; phase change; male sterility;
 KW KW hybrid seed production; herbage quality; early maturing crop;
 KW KW biomass increase; branching increase; blocking flowering;
 KW KW allergenic pollen; floral meristem identity protein; gene; ss.

XX OS Lolium perenne.

XX PN WO200233091-A1.

XX PD 25-APR-2002.

XX PF 17-OCT-2001; 2001WO-AU001311.

XX PR 19-OCT-2000; 2000AU-00000873.

XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX FA (AGRE-) AGRESEARCH LTD.

XX XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;

XX XX WPI; 2002-454601/48.

XX DR P-PSDB; ABG60941.

XX XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.

XX PS Claim 3; Fig 54; 290pp; English.

XX CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant

CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced biomass in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles

XX SQ Sequence 979 BP; 305 A; 236 C; 246 G; 192 T; 0 U; 0 Other;

Query Match 29.6%; Score 256.8; DS 6; Length 979;

Best Local Similarity 64.4%; Pred. No. 5e-55;

Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 1 ATGGAGCGTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGAGGTGACC 60
 Db |||||
 QY 134 ATGGGGCGGGGAAGATCGAGATCAAGAGGATCGAAGACCAAGAGCAACGCCAGGTGACC 193
 Db |||||
 QY 61 TACTCAAGAGGAGGAATGGGATTATCAAGAGGCAAGAGGAGATCACTGTTCTATGTGAT 120
 Db |||||
 QY 194 TTCTCCAGCGCAAGACGGGATCTCAAGAGGCCAAGGAGATCAGCGTGTCTCGGAC 253
 Db |||||
 QY 121 GCTAAGATATCTTTATCATTTATTTCTAGCTCTGGGAAGATGGTTGAATATCTGACGCCCT 180
 Db |||||
 QY 254 GCGGAGGTGCGCGTGTCTCTCTCCAGCGCGCAAGCTCTACGACTTCTGCTCCCC 313
 Db |||||
 QY 181 TCAACTAGCTGACAGAAATCTTGACAAATACCATGGACAACTTGGGAAGAAGTTGTGG 240
 Db |||||
 QY 314 AAGACATCGTATCAAGATCTTGGGAAGTACCAAGCAACTCCGGGAAGATCTGTGG 373
 Db |||||
 QY 241 GATGCTAAGCATGAGAACTCAGCAATGAAGTGGATAGAGTCAAGAAAGCAATGACAGC 300
 Db |||||
 QY 374 GATGAGAAACACAGAGGCTCAGCGCGGAGATTGATCGAATCAAGAAAGAAATGATAAC 433
 Db |||||
 QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGGAGGATATCACATCTTGAACCATGTAGAG 360
 Db |||||
 QY 434 ATGCAGATCGAGCTCAGGCATCTTGAAGCGGAAGATCTGAATCTACTGCAACCCAAAGAG 493
 Db |||||
 QY 361 CTGATGGCCTTAGAGGAAGCACTTGAAATGGCCCTTACAAGTATCCGGGACAGCAGTCC 420
 Db |||||
 QY 494 TTGATCATGATTGAGGAAGCACTTGTATATGAGCTGACAGGCTGTCATGAAAAACAGATG 553
 Db |||||
 QY 421 AAGTTCTCGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATAAGCGCCTC 480
 Db |||||
 QY 554 GAGCACTACGACAGGCTGATGAAACTGGCAGATGCTAGAAGATGAGAACTAGTTGCTC 613
 Db |||||
 QY 481 ACTTATGAGCTGCAAAACACAGGAGATGAAATTAAGAGAAATGTGAGAAACATGGAA 540
 Db |||||
 QY 614 GCATTTAACTGC---ATCAGCAAGATATTGCGCTGACCGGAAACATGAGGAGCTTGAG 670
 Db |||||
 QY 541 AATGGGTATCATCAGAGGAGCTGGGGAATCTAACAAACAAACACAGCAGCAGATACCTTTT 600
 Db |||||
 QY 671 CTTGTTTACCATCG-----GACAGGGACTTTTGCAGGCCAGATGCGGATC 715
 Db |||||
 QY 601 GCCTTCGGCTGAGCCTTATTCAGCCAAATCTCCAGGAGAGATCTTAATAGATATATCT 660
 Db |||||
 QY 716 ACGTTCCGCTGCGACCTAGCCACCACTGCGAGGAGAACAGCTAGGCGCTTTAATCT 775
 Db |||||

RESULT 12

ABK82127
 ID ABK82127 standard; cDNA; 1065 BP.
 XX
 AC ABK82127;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE DNA encoding novel floral meristem identity protein LpMADS2-3.
 XX
 KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; gene; ss.
 XX
 OS Lolium perenne.
 XX
 XX WO200233091-A1.
 XX
 PD 25-APR-2002.
 XX
 XX 17-OCT-2001; 2001WO-AU001311.
 PF
 XX 19-OCT-2000; 2000AU-00000873.
 XX
 PR (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX
 PA (AGRE-) AGRESEARCH LTD.
 XX
 XX Spangenberg G, Sawbridge TI, Ong EK, Emermerling M;
 FI WPI; 2002-454601/48.
 XX
 DR P-PSDB; ABG60945.
 XX
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 FT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 PS Claim 3; Fig 72; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (i), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral

meristem identity protein involved in floral development and a potential
 target for manipulating plant life cycles
 CC
 XX
 SQ Sequence 1065 BP; 327 A; 254 C; 268 G; 216 T; 0 U; 0 Other;
 Query Match Similarity 29.6%; Score 256.8; DB 6; Length 1065;
 Best Local Similarity 64.4%; Pred. No. 5.2e-55;
 Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;
 QY 1 ATGGGAGCTGGGAAGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGCAGGTGACC 60
 DB 128 ATGGGGCTGGGAAGATCGAGATCAAGAGGATCGAGAAACAGAGCAACCCAGGTGACC 187
 QY 61 TACTCCAAGAGGAGGATGAGATATCAAGAGGCAAGGAGATCACTGTTCTATGTGAT 120
 DB 188 TTCTCCAAGCGCAAGACGGGATCTCAAGAGGCGCAAGGAGATCAGCGTGCTCTGGCAG 247
 QY 121 GCTAAAGTATCTCTTATCATTTATTCTAGCTCTGGGAAGATGGTTGAATACTGACGCCCT 180
 DB 248 GCCAGGTGGCGCTGCTGCTTCTCCAGCGCGGCGAGCTCTACGACTTCTGCTCCCA 307
 QY 181 TCAACTACGTGACAGAAATCTTGGACAAATACCATGGACAATCTGGGAAGAGTTGTGG 240
 DB 308 AAGACATCGCTATCAAGAATCTTGGAGAAGTACCAGACCAACTCCGGGAAGATCTGTGG 367
 QY 241 GATGTAAGCATGAGAAACCTCAGCAATGAAGTGTAGATGATCAAGAAAGCAATGACAGC 300
 DB 368 GATGAGAAACACAAGAGCTCAGTGGCGAGATTGATCGAATCAAGAAAGAAATGACAC 427
 QY 301 ATGCAAGTAGAGCTCAGGCATCTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 DB 428 ATGCAGATCGAGCTCAGCACTTGAAGGCGCAAGATCTGAATCACTGCAACCAAGAG 487
 QY 361 CTGATGGCTTAGAGGAGCACTTGAAGTGGCTTACAGTATCCGGGACAGCAGTCC 420
 DB 488 TTGATCATGATTGAGGAAGCACTTGAATGAGCTGACAGGCTGCGATGAAGAAACAGATG 547
 QY 421 AAGTTCTGCATCATGACAGACAATGGAAGGCACTGGAAGATGAGAATAAGCGCTC 480
 DB 548 GAGCATTACGACAGCTGATGAAATGCGCAAGATGCTAGAAGATGAGAACTAGTTGCTC 607
 QY 481 ACTTATGAGCTGCAAAAACAACAGGAGATGAAATAAAGAGATGTGAGAAACATGGA 540
 DB 608 GCATCTAAACTGC---ATCAGCAAGATATTGCGCTGAACCGGGAACATGAGGAGCTTGAG 664
 QY 541 AATGGGTATCATCAGAGGAGCTGGGAACTTACAAACAACCAACAGCAGCAGATACCTTTT 600
 DB 665 CTGGTTACCATCG-----GACAGGAGACTTTGCGAGCCACATGCCGATC 709
 QY 601 GCCTTCGCGTGCAGCTTATTCAGCCAAATCTCCAGGAGAGATCTAATTAGATATATCT 660
 DB 710 ACGTTCCGCTGCAGCTAGCCCAACCTCGAGGAGAACAGCTAGGCGGCTTTAATCT 769
 RESULT 13
 AAC35208
 ID AAC35208 standard; DNA; 909 BP.
 XX
 AC AAC35208;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 9372.
 XX
 KW Hybridisation assay; Genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126284P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130499P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
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Best Local Similarity 63.0%; Pred. No. 6e-50;
Matches 402; Conservative 0; Mismatches 227; Indels 9; Gaps 2;
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 Db 223 TTCTCCAGCGCGCGGCGGACTGGTCAAGAGGCAAGGAGATCGGCGTCTCTCGAC 282
 Qy 121 GCTAAAGTATCTTATCATTTATTTAGTCTCTGGAGAGATGTTGAATCTGACGCCCT 180
 Db 283 GCCGAGTCCGCGCGCGTCTCTTCCAGCGCGGCGAGCTCTATGACTACTCTCGCCC 342
 Qy 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACATGGCAATCTCGGAAGATTTGTGG 240
 Db 343 AGGACCTCGTGTCCAGATCTTGGAGATCAAGACCACTCCGGGAGATTTGTGG 402
 Qy 241 GATGCTAAGATGAGAACCTTCAGCAATGAAGTGAATGATCAAGAAAGACAAATGACAGC 300
 Db 403 GGTGAGAGGACCAAGAACCTTGAGTCAGAGATCGACAGAGTCAAGAGGAGAACGACAA 462
 Qy 301 ATGCAAGTACAGCTCAGGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 Db 463 ATGCAAGTACAGCTCAGGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 522
 Qy 361 CTGATGCGCTTAGAGGAGCACTTGAAGTGGCTTTACAGTATCCGGGACAGCAATGCC 420
 Db 523 CTGATGCGCTTAGAGGAGCACTTGAAGTGGCTTTACAGTATCCGGGACAGCAATGCC 582
 Qy 421 AAGTTCGTCACATGATGAGACATGGAAGGCACTGGAATGAGATGAGATGAGCCCTC 480
 Db 583 GACTACTGAGAGTGCACAGCAATGGAAGTGGAGATGCTGGAGGACCAATAGATAC 642
 Qy 481 ACTTATGAGTGCACAAACACAGGAGATGAAATGAAAGAGAAATGTGAGAAACATGAA 540
 Db 643 ACTTTAGATGC---ACCAACAGGCTGTTGATCTGAGCGGCGCATGAGGAGCTGGAG 699
 Qy 541 AATGGGTATCATGAGGAGGAGCTGGGAACTACAAACAAACAGCAGCAGATACCTTTT 600
 Db 700 ACCGGATACCATCAGGTCCAGC-----ACGACAGGGATTTCAATTTCCAGATGCCGTT 753
 Qy 601 GCCTTCGCGTGCAGCTATTTCAGCCAAATCTCCAGGA 638
 Db 754 ACCTTCGGGTGAGCCACCAACCACTCCACCTGCAGGA 791

RESULT 15

ABK82090
 ID ABK82090 standard; cDNA; 592 BP.

AC ABK82090;

XX 27-AUG-2002 (first entry)

DE Novel floral meristem identity gene LpMADS1 contig #5.

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTFORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.

OS Lolium perenne.

XX FN W020023091-A1.

XX 25-APR-2002.

XX 17-OCT-2001; 2001WO-AU001311.

XX 19-OCT-2000; 2000AU-00000873.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

(AGRE-) AGRESEARCH LTD.
 Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 WPI; 2002-454601/48.
 New substantially purified or isolated polypeptide e.g., MADS-box,
 CENTFORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 fescue species, useful for controlling plant life cycles and/or growth
 phases.

Claim 3; Fig 29; 290pp; English.

The invention describes a substantially purified or isolated polypeptide
 (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 MADS-box (MADS) and MADS-like proteins, CENTFORADIALIS (CEN) and CEN-like
 proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 and HB-like proteins, or their functionally active fragments or variants.
 Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 vector (IV) comprising (II), is useful for modifying plant life cycles
 and/or growth phases, flowering processes, flowering and/or plant
 architecture and/or flower and/or inflorescence development in a plant,
 which involves introducing (II), (III) or (IV) into the plant. The
 individual or simultaneous enhancement or downregulation of MADS-box gene
 activities may alter flower, embryo and seed development, e.g., enhance
 or inhibit embryo differentiation and growth or alter flower organ
 identity through conversion of one floral organ in another. Manipulation
 of CEN or HB activity in plants alters the control of phase change,
 flowering time and the number of leaves made before flowering.
 Manipulation of AP2 activity in plants alters flower organ identity
 through conversion of one floral organ in another, leads to a change in
 the number of floral organs and flowering architecture. Manipulation of
 flowering plant architecture has a wide range of applications such as:
 inducing male sterility for hybrid seed production; changing flower
 architecture for enhancing value of ornamentals; delaying flowering in
 forage grasses thus stopping the formation of less digestible stems and
 increasing herbage quality; altering flowering time allowing early
 maturing crops; delaying vegetative phase to increase biomass production;
 increasing branching to enhanced business in fruit trees; altering plant
 size e.g. shorter plant stature; and in blocking flowering and reducing
 release for allergenic pollen. This sequence represents a contig
 polynucleotide novel floral meristem identity protein involved in floral
 development and a potential target for manipulating plant life cycles

Sequence 592 BP; 177 A; 143 C; 161 G; 95 T; 0 U; 16 Other;
 Query Match 27.2%; Score 236; DB 6; Length 592;
 Best Local Similarity 66.7%; Pred. No. 7.9e-50;
 Matches 329; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTTGAGAACTCAAGTAAACGAGGAGTGAAC 60
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 Qy 61 TACTCCAGAGGAGGATGAGATATCAAGAGGCAAGAGAGATCACTGTTCTATGTAT 120
 Db 144 TTCTCCAGGCGCAAGAACCGGATCCTCAAGAGGCCCAAGAGAGATCAGCGTCTCTCGAC 203
 Qy 121 GCTAAAGTATCTTATCATTTATTTAGCTCTGGGAAGATGTTGAATACTGACGCCCT 180
 Db 204 GCCGAGTGGCGTCTGCTGCTTCTCCAGCGCGGCAAGCTCTACGACTCTGCTCCCC 263
 Qy 181 TCAACTACGCTGACAGAAATCTTGGACAAATACCATGAGCAATCTCGGAGAAAGTTGTGG 240
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 Qy 241 GATGCTAAGCATGAGAACCTTCAGCAATGAGTGGATAGAGTCAAGAGAAACATGACAGC 300
 Db 324 GATGAGAAACACAGAGGCTCAGCGGAGATTTGATGATCAAGAGAGAAATGATGATAC 383
 Qy 301 ATGCAAGTACGCTCAGGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 Db 384 ATGCAATGAGCTCAGGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 443

QY	361	CTGATGGCCTTAGAGGAGCACTTGAAAATGGCCTTACAAGTATCCGGGACAAGCAGTCC	420
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QY	421	AAGTTGTCGACATGATGAGAGACAAATGGAAAGGCACCTGGAAGATGAGAATTAAGCGCCTC	480
Db	504	GAGCACTACNACAGGCTGATGAATACTGCNNGATGCTNNAAGATGANAACAAGTGTTC	563
QY	481	ACTTATGAGCTGC	493
Db	564	GNATTTAAACTGC	576

Search completed: September 25, 2004, 16:09:50
Job time : 406.034 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 14:17:32 ; Search time 3666.24 Seconds
(without alignments)
10261.660 Million cell updates/sec

Title: US-10-069-527-1
Perfect score: 868
Sequence: 1 atgggacg9ggaaggttga.....aaaaaaaaaaaaaaaaaaaaa 868

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba.*
2: gb_btg.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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16: em_fun.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	868	8	MDO291490
2	768.2	88.5	890	8	AJ291490 Malus dom
3	358.8	41.3	967	8	AB081092 Malus x d
4	354.8	40.9	845	8	AB038462 Rosa rugo
5	354.2	40.8	875	8	AF043255 Cucumis s
6	350	40.3	3130	8	BPE488589 Betula pe
7	323.4	37.9	904	8	MDO291491 Malus dom
8	323.4	37.9	971	8	XJ1417 P.hybrida f
9	296.8	34.1	761	8	X69947 P.hybrida m
10	296.8	34.1	761	8	X69947 P.hybrida m
11	291.4	33.6	780	6	AT230711 Hydrangea
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13	288.4	33.2	814	8	AY173061 Chrysanth
14	280.2	32.3	920	8	AF029976 Eucalyptu
15	278.8	32.1	807	8	AB079259 Agapanthu
16	277.2	31.9	810	8	AB079259 Gerbera h
17	274.6	31.6	802	8	GHY9726 Delphinu
18	274.2	31.6	876	8	AF052862 Tulipa ge
19	274	31.6	848	8	AB094967 Helianthu
20	273.4	31.5	894	8	AY173069 DCA271148
21	267.6	30.8	896	8	AF052857 Dicentra
22	267.6	30.8	896	8	SLSLM2
23	267.4	30.8	801	8	AF335473
24	267.2	30.8	784	8	AY162865 Cimicifug
25	266	30.6	896	8	AY162861 Berberis
26	265.2	30.6	896	8	ATHMADSBOX
27	264.6	30.5	759	8	AF052861 Syringa v
28	264.6	30.5	959	8	AF230710 Chloranth
29	259.8	29.9	744	8	AF230708 Calycanth
30	259	29.8	822	8	AB071379 Lilium re
31	258	29.7	697	8	AY157725 Helianthu
32	256.6	29.6	786	8	AY162836 Akebia qu
33	256.4	29.5	793	8	AY162860 Berberis
34	256	29.5	790	8	AY162866 Cimicifug
35	253.6	29.2	810	8	AY162837 Akebia qu
36	252.2	29.1	791	8	AF052863 Michelia
37	250	28.8	909	8	AF089002 Arabidops
38	249	28.7	800	8	AF30713 Tacta cha
39	247.2	28.5	733	8	AF052864 Liriodend
40	244.2	28.1	801	8	AB071380 Lilium re
41	242.2	27.9	907	8	AB094985 Orchis it
42	239	27.5	888	8	AF134114 Hyacinthu
43	237	27.3	719	8	AB089155 Houttuyni
44	235.8	27.2	768	8	AY162867 Cimicifug
45	235.8	27.2	879	8	AF134115 Hyacinthu

ALIGNMENTS

RESULT 1
MDO291490

LOCUS Malus domestica mRNA for Pistillata MADS-box protein (pi Gene).
DEFINITION MDO291490 868 bp mRNA linear PLN 02-FEB-2001

ACCESSION AJ291490
VERSION AJ291490.1 GI:12666532
KEYWORDS PI gene; Pistillata MADS-box protein.
SOURCE Malus x domestica (apple tree)
ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids i; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1
AUTHORS Yao,J., Dong,Y. and Morris,B.A.
TITLE Parthenocarpic apple fruit production conferred by transposon

Pred. No. is the number of results predicted by chance to have a

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

insertion mutations in a MADS-box transcription factor
Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1306-1311 (2001)
21107711
11158635
2 (bases 1 to 868)
Yao, J.L.
Direct Submission
Submitted (16-OCT-2000) Yao J.L., Plant Health and Development
Group, Horticulture and Food Research Institute of New Zealand, 120
Mt Albert Road, Auckland, Private Bag 92169, NEW ZEALAND

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 868; DB 8; Length 868;
Best Local Similarity 100.0%; Pred. No. 3.6e-208;
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACGCTGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGCGAGTGACC 60
DB 1 ATGGACGCTGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGCGAGTGACC 60

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DB 61 TACTCCAGAGGAGGATGGATTATCAAGAGGCAAGGAGATCACTCTTCTATGTGAT 120

QY 121 GCTAAAGTATCTCTTATCAATTTATCTAGCTCTGGGAAGATGTTGAATPACTGCAGCCCT 180
DB 121 GCTAAAGTATCTCTTATCAATTTATCTAGCTCTGGGAAGATGTTGAATPACTGCAGCCCT 180

QY 181 TCACTACGCTGCAGAAATCTTGGCAATATCAAGAGGCAAGGAGATCACTCTTCTATGTGAT 240
DB 181 TCACTACGCTGCAGAAATCTTGGCAATATCAAGAGGCAAGGAGATCACTCTTCTATGTGAT 240

QY 241 GATGCTAAGCATGAGAACTCAGCAATGAAGTGGATAGAGTCAAGAAAGACATGACAGC 300
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DB 361 CTGATGCGCTTAGAGGAAGCACTTGAATATGCGCTTACAGATATCCGGACAGCAGTCC 420

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DB 661 TGCATTTCATGCTCTTTCTAACTAGTATTATATATCTCCACCTCTCTCTCTTTCA 720
QY 721 TCTGTCAAGGAGTCTTAAAGTTTATGTCAGATTTCCAAATGGTTTGTAAATGAATAGCTT 780
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QY 781 CGTTATGAGGCTTTGTTGTGAACCTTGTAAATTAAGGGGTGCATGAACCTCGGTTTGTG 840
DB 781 CGTTATGAGGCTTTGTTGTGAACCTTGTAAATTAAGGGGTGCATGAACCTCGGTTTGTG 840
QY 841 GCAAAAAA 868
DB 841 GCAAAAAA 868

RESULT 2

AB081092

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

ORIGIN

Query Match

Score 768.2; DB 8; Length 890;

Best Local Similarity 99.0%; Pred. No. 5.6e-183;		
Matches 773; Conservative 0; Mismatches 8; Indels 0; Gaps 0;		
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Db		
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Db		
QY	195 AGAAATCTTGGACAAATAACCATGGACAAATCTGGGAAGAAATTGTGGATGCTTAAGCATGA	254
Db		
QY	121 AGAAATCTTGGACAAATACCATGGACAAATCTGGGAAGAAATTGTGGATGCTTAAGCATGA	180
Db		
QY	255 GAACTCTCAGCAATGAAGTGGATGAGTCAAGAAAGCAATGACAGCATGCCAAGTAGAGCT	314
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QY	181 GAACTCTCAGCAATGAAGTGGATGAGTCAAGAAAGCAATGACAGCATGCCAAGTAGAGCT	240
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QY	315 CAGGCATCTGAAGGGAGAGGATATCACATCATTTGAACCATGTAGAGCTGATGGCCTTAGA	374
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QY	375 GGAAGCATTGAAATGGCCCTTCAAGTATCCGGGACAGACGATCCCAAGTTCGTGCGACAT	434
Db		
QY	301 GGAAGCATTGAAATGGCCCTTCAAGTATCCGGGACAGACGATCCCAAGTTCGTGCGACAT	360
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QY	435 GATGAGAGCAATGGAAGAGGCACCTGGAAGATGAGAATAAGCGCCTCACTTATGAGCTGCA	494
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QY	421 AAAACAAACGAGAGATGAAATTAAGAAAGAAATGTGAGAAACATCGGAAATGGGTATCATCA	480
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QY	555 GAGGACGCTGGGGAATCAACAACAACCCAGCAGCATACCTTTTGCCTTCGCGTGCA	614
Db		
QY	481 GAGGACGCTGGGGAATCAACAACAACCCAGCAGCATACCTTTTGCCTTCGCGTGCA	540
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QY	615 GCCTATTAGCCAAATCTCCAGGAGAGAAATCTAATTAGATATATCTTGCAATTTGCAATGCT	674
Db		
QY	541 GCCTATTAGCCAAATCTCCAGGAGAGAAATCTAATTAGATATATCTTGCAATTTGCAATGCT	600
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QY	675 CTTTCTAACTAGTTATATTATCTCTCCACCTCTCTCTCTTTTCATCTGTCAAGGAGTT	734
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QY	601 CTTTCTAACTAGTTATATTATCTCTCCACCTCTCTCTCTTTTCATCTGTCAAGGAGTT	660
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QY	735 CTTAAGTTTATGTGAGATTTCMAATGGTTTGTAAATGGAATAGCTTCGTTATGAGGCTTT	794
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QY	661 CTTAAGTTTATGTGAGATTTCMAATGGTTTGTAAATGGAATAGCTTCGTTATGAGGCTTT	720
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QY	795 GTTGTCAAACCTTGTAATAATTAAAGCGGTGCATGAACCTCGGTTGTGGGAAAAAATAAAAA	854
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QY	721 GTTGTCAAACCTTGTAATAATTAAAGCGGTGCATGAACCTCGGTTGTGGGAAAAAATAAAAA	780
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QY	855 A 855	
Db	781 A 781	

RESULT 3	
AB038462	
LOCUS	Rosa rugosa MASAKO BP mRNA for MADS-box protein, complete cds.
DEFINITION	
ACCESSION	AB038462
VERSION	AB038462.1 GI:9857311
KEYWORDS	MASAKO BP; MADS-box protein.
SOURCE	Rosa rugosa
ORGANISM	Rosa rugosa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosoids I; Rosales; Rosaceae; Rosoideae; Rosa. 1

AUTHORS Kitahara K., Hirai, S., Fukui, H. and Matsumoto, S.
TITLE Rose MADS-box genes 'YASAKO BP and B3' homologous to class B floral identity genes
JOURNAL Plant Sci. 151, 549-557 (2001)
REFERENCE 2 (bases 1 to 967)
AUTHORS Matsumoto, S., Hirai, S. and Kitahara, K.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) Shogo Matsumoto, Gifu University, Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu, Gifu 501-1193, Japan (E-mail:shmatsumoc@gifu-u.ac.jp, Tel:+81-58-293-2257. Fax:+81-58-293-2207)

FEATURES
SOURCE

gene

cps

polyA site

ORIGIN

Query Match	41.3%	Score 358.8;	DB 8;	Length 967;
Best Local Similarity	76.4%	Pred. No. 1.1e-79;		
Matches 498.	Conservative	0;	Mismatches 112;	Indels 42;
				Gaps 3;

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Db	164	TATTCTAAGAGAAGAATGGGATCATCAAAAAGGCTAAGGAAATCACTGTTCTTTGTGAT	223
QY	121	GCATAAGTATCTCTTATCATTTATCTPAGCTCTGGGAAAGTGGTTGAATACTGCA---GC	177
Db	224	GCTAAGGTTTCTCTTATATCATTTGCTTAGCTCTGGAAAAATGGTTGAATACTGCAGCGGC	283
QY	178	CCTTCAACTACGCTGACAGAAAATCTTGGACAAATACCATGGACAATCTGGGAAAGAATTG	237
Db	284	CCTCAGGAAACGCGGATGAAAATCTTGGACAAATACCACCTCACAGTCTGGAAAGAGGTTA	343
QY	238	TGGGATGCTAAGCATGATGAACCTCAGCAATGAAGTGGATGATAGGTCAAGAAGACAATGAC	297
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Db	404	GGCATGCAAAATTGAGCTTCGGCATTTGAAGGGGGAAGACATAACATCTCTGAACCATGTG	463
QY	358	GAGCTGATGGCCTTTAGAGGAGACACTTGAAAATGGCCTTACAAGTATCCGGGACAAGCAG	417
Db	464	GACCTGATGGCCTTTAGAGGAGCAATTGAAAATGGCCTTCCAAGTATCAGAGACAGAATG	523
QY	418	TCCAAGTTGCTGCATGATGAGAGACAAATGGAAAGGCACTGGAAAGATGAGAAATAGGCG	477
Db	524	TCGAAGTACATGGACGCGGTTAGAGAAAATAACAGAGCTCTGGAGGAGCAGAAATAGCGC	583
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Db      584 CTCGATATCAGTGCACAAA-----ATGATGAATCTGAAGAGAAATTTGAGGACATG 637
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Db      638 -----NACTACACACACACACTCAGATACCT 664
Qy      598 TTTCCTTCCCGTGCAGCCTATTTCAGCAAAATCTCAGAGAGAAATCTTAAT 649
Db      665 TTTCCTTACGTGTCAGCCTTAATCAGCAAAATCTCAGCAGCAATGTAAT 716

RESULT 4
AF043255
LOCUS      Cucumis sativus MADS box protein 26 (CUM26) mRNA, complete cds.
DEFINITION
ACCESSION AF043255
VERSION    AF043255.1 GI:4105096
KEYWORDS
SOURCE     Cucumis sativus (cucumber)
ORGANISM   Cucumis sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE 1 (bases 1 to 845)
AUTHORS   Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and
          Angenent,G.C.
TITLE     Class C homeotic genes are required for whorl specific sex
          determination in unisexual flowers
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 845)
AUTHORS   Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and
          Angenent,G.C.
TITLE     Direct Submission
JOURNAL   Submitted (15-JAN-1998) Developm. Biology, CPRO-DLO,
          Droeveendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
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        6 ATGGGAGAGGAGGAAATAGAAATAAAAGAAATAGAGAACTCAAGCAATAGACAAGTTACA 65
          |||||
        61 TACTCAAGAGAGGAGGAGGATTATCAAGAGGCAAGGAGAGTCACTGTTCTTATGTGAT 120
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        66 TATTCAAGAGAGAGAAATGGTATCATCAAAAAGCCAAAGAAATTAAGTTCTTTGGCAT 125
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        121 GCTAAAGTATCTTATCATTTTATTCTAGCTCTGGGAGAGATGGTTGAATCTGACGCCCT 180
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Db      126 GCTCAAGTTTCTTGTTCATTTTGTCTAGCTCTGGAAAAATGTCATGAATATTGACGCCCT 185
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Qy      661 TGCATTTGCATGCTCTTTCTAACTAGTTATATATATCTCTCCACCTCTCTCTCTTTTCA 720
Db      654 TATAT---CTATTTCTCTTTATGTTTATGTTTATGTTTATGTTTATGTTTAT 710
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Db      826 ATAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 845

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RESULT 5
BPE48589
LOCUS      Betula pendula mRNA for PISTILLATA homologue (mads2 gene).
DEFINITION
ACCESSION AJ488589
VERSION    AJ488589.1 GI:28874429
KEYWORDS   mads2 gene; PISTILLATA.
SOURCE     Betula pendula (European white birch)
ORGANISM   Betula pendula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fagales; Betulaceae; Betula.
REFERENCE 1
AUTHORS   Jarvinen,P., Lemmetyinen,J., Savolainen,O. and Sopanen,T.
TITLE     DNA sequence variation in BpMADS2 gene in two populations of Betula
          pendula
JOURNAL   Mol.Ecol. 12 (2), 369-384 (2003)
MEDLINE   22423798
PUBMED    12535088
REFERENCE 2 (bases 1 to 875)
AUTHORS   Jaervinen,P.L.H.
TITLE     Direct Submission

```

JOURNAL Submitted (29-MAY-2002) Jaervinen P.L.H., Biology, University of Joensuu, P.O.Box 111, FIN-80101, Joensuu, FINLAND

FEATURES

source

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/db_xref="taxon:3505"

/sex="male"

/tissue_type="inflorescence"

/country="Finland"

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/product="PISTILLATA homologue"

/protein_id="CAD32764.1"

/db_xref="GI:28874430"

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ORIGIN

Query Match 40.8%; Score 354.2; DB 8; Length 875;

Best Local Similarity 73.0%; Pred. No. 1.7e-78;

Matches 474; Conservative 0; Mismatches 163; Indels 12; Gaps 1;

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Db 1 ATGGGAGGAAAGATAGAGATAAGAGAGATAGAGAACTCAAGTAACAGGAGGTGACC 60

QY 61 TACTCCAAGAGGAGGAATGGGATATCAAGAGGCAAGAGATCACTCTTATGTGAT 120

Db 61 TACTCCAAGAGGATGAAGGGGATCATAAAGAGAGGCTAAGAGATGACGATTCATGTGAT 120

QY 121 GCTAAAGTATCTCTTATCATTTATCTAGCTCTGGGAAGATGTTGTAATCTGCACCCCT 180

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Db 301 ATGCAAGTTGAATCAGGCATGAGAGGAGGAGATATCATCATTTGAACCAATGAGAG 360

QY 361 CTGATGCCCTTAGAGGAGCACTTGAATAATGGGCTTACAGATATCCGGACACGAGTCC 420

Db 361 CTGATGATCCTTGAAGAGGCTTCAAAATGGCCACAGCAGATATCCCGGAGGCGAGATG 420

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Db 481 AATTTCACCTCTGCATCAGCAGCAGATGGCGATGGAAGCAGCAGCTGCAGAGACGTGGAA 540

QY 541 AATGGGTATCATCAGAGCAGCTGGGGAATCTACACACACACACAGCAGCAGATACCTTTT 600

Db 541 GATGATATGAGCAGAGGAGGTGAGG-----ACTATAATCTCAATATGCCCTTTT 588

QY 601 GCCTTCCGCGTGCAGCCTATTTCAGCCAAATCTCAGGAGAGAAATCTAAT 649

Db 589 GCTTTCGCGTGCAGCCTATTTCAGCCAAATCTCAGGAGATGATGTAAT 637

RESULT 6

MDO291491 3130 bp DNA linear PLN 02-FEB-2001

LOCUS

DEFINITION Malus domestica pi gene for Pistillata MADS-box protein, exons 1-7.

ACCESSION AJ291491

VERSION AJ291491.1 GI:12666534

KEYWORDS PI gene; Pistillata MADS-box protein; transcription factor.

SOURCE Malus x domestica (apple tree)

ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids 1; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1

Yao, J., Dong, Y. and Morris, B.A. Parthenocarpic apple fruit production conferred by transposon insertion mutations in a MADS-box transcription factor Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1306-1311 (2001)

JOURNAL MEDLINE 21107711

PUBMED 11158635

REFERENCE 2 (bases 1 to 3130)

Yao, J.L. Direct Submission

Yao, J.L. Submitted (16-OCT-2000) Yao J.L., Plant Health and Development Group, Horticulture and Food Research Institute of New Zealand, 120 Mt Albert Road, Auckland, Private Bag 92169, NEW ZEALAND

Location/Qualifiers

1..3130

/organism="Malus x domestica"

/mol_type="genomic DNA"

/cultivar="Granny Smith"

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1473..1775

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mrna

CDS

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1806..1915
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ORIGIN
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Best Local Similarity 98.6%; Pred. No. 2e-77;
Matches 353; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 483 TTATGAGCTCAAAACACAGAGAGATGAAATAAAGAGAGATGTCAGAAACATGCAAAA 542
Db 2773 TGAATTCGACAAACACAGAGAGATGAAATAAAGAGAGATGTCAGAAACATGCAAAA 2832

Qy 543 TGGGTATCATCAGAGGAGCTGGGGAACCTACAAACAACACAGCAGATACCTTTTGC 602
Db 2833 TGGGTATCATCAGAGGAGCTGGGGAACCTACAAACAACACAGCAGATACCTTTTGC 2892

Qy 603 CTTCGGGTGAGCTTATCAGGCAATCTCCAGGAGAGATCTAATATAGATATATCTTG 662
Db 2893 CTTCGGGTGAGCTTATCAGGCAATCTCCAGGAGAGATCTAATATAGATATATCTTG 2952

Qy 663 CATTTGATGCTCTTTCTAACTAGTTATATATCTCTCACTCTCTCTCTCTCTCTCTC 722
Db 2953 CATTTGATGCTCTTTCTAACTAGTTATATATCTCTCACTCTCTCTCTCTCTCTCTC 3012

Qy 723 TGTCAAGAGTCTTTAAGTTATGTCAGATTTCCAAATGTTTGTATGAATAGCTTCG 782
Db 3013 TGTCAAGAGTCTTTAAGTTATGTCAGATTTCCAAATGTTTGTATGAATAGCTTCG 3072

Qy 783 TTATGAGGCTTCTGTTGAACCTTGTAAATAATTAAGCGCTGATGAACCTCGGTTTGTG 840
Db 3073 TTATGAGGCTTCTGTTGAACCTTGTAAATAATTAAGCGCTGATGAACCTCGGTTTGTG 3130

RESULT 7
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LOCUS      P.hybrida fbp3 mRNA.          904 bp      mRNA      linear      PLN 10-FEB-1994
DEFINITION X71417
ACCESSION  X71417
VERSION    X71417.1 GI:454264
KEYWORDS   fbp3 gene; MADS-box protein.
SOURCE     Petunia x hybrida
ORGANISM   Petunia x hybrida
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamids; Solanales; Solanaceae; Petunia.

REFERENCE
AUTHORS    Angenent,G.C.; Franken,J.; Busscher,M.; Weiss,D. and van Tunen,A.J.
TITLE      Co-suppression of the petunia homeotic gene fbp2 affects the
            identity of the generative meristem
JOURNAL    Plant J. 5 (1), 33-44 (1994).
MEDLINE    9417174
PUBMED     7907515
REFERENCE  2 (bases 1 to 904)
AUTHORS    Angenent,G.C.
TITLE      Direct Submission
JOURNAL    Submitted (30-MAR-1993) G.C. Angenent, CPRO-DLO, Droeendaalsesteeg
            1, Wageningen, THE NETHERLANDS
FEATURES   Location/Qualifiers

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Query Match      37.9%; Score 329.4; DB 8; Length 904;
Best Local Similarity 70.6%; Pred. No. 3e-72;
Matches 457; Conservative 0; Mismatches 181; Indels 9; Gaps 1;

Qy 1 ATGGGAGCTGGCAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGAGGTGACC 60
Db 46 ATGGGAGAGGAAGATAGAGATTAAGAGATAGAGACTCTAGCAACAGGCAAGTTACT 105

Qy 61 TACTCCAAAGAGAGGAATGGGATTATCAAGAGGCAAAAGGAGATCACTGTTTCTATGTAT 120
Db 106 TACTCCAAAGAGAGGAATGGGATTATCAAGAGGCAAAAGGAGATCACTGTTTCTATGTAT 165

Qy 121 GCTAAAGTATCTCTTATCATTTTCTAGCTCTGGGAAGATGTTGAATATCTGACGCCCT 180
Db 166 GCTAAGGTTTCCCTTATCATCTTTGGTATTCCTGGCAAGATGATGATATTTGACCCCT 225

Qy 181 TCAACTACGTGACAGAAATCTTGGACAAATACCATGGACAATCTGGGAAGAGTTGTGG 240
Db 226 TCTACTACGTGATCTGATATGCTGGATGTTATCAAAAACCTCTGGGAGAGGCTATGG 285

Qy 241 GATGCTAAGCATGAGACCTCAGCAATGAGTGGATAGTAGTCAAGAAACACATGACAGC 300
Db 286 GATGCTAAGCATGAGAACTTGAACAATGAATCGATAGAAATCAAGAAAGAGAACGACAGT 345

Qy 301 ATGCAAGTAGAGCTCAGGCACTCTGAAGGGAGAGGATATCACATCATTTGAACCATGTAGAG 360
Db 346 ATGCAAGTTAAGCTCAGGCACTCTGAAGGAGAGATATCAATTTCTTTGAACCAACAAGAG 405

Qy 361 CTGATGCGCTTAGAGGAGCACTTGAATATGCGCTTACAGATATCCGGGACAGAGCTCC 420
Db 406 CTTATGGTTTGGGAAGAGGCTTAAACAATGGACTTTCTAGTATCAGTCCCAAGAGCTCG 465

Qy 421 AAGTTCTGTCACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGAAATAGCGCCCTC 480
Db 466 GAGATCTTGAGGATAGTCAGGAATAATGATCAAAATCTTGGAGAGGAAACACAGCAACTT 525

Qy 481 ACTTATAGCTGCAAAAACACAGGAGATGAATAAAGAGAAATGTGAGAAACATGGAA 540
Db 526 CAATATGCTTTGACCAAAAGGAGATGGCAGCCATGGGTGGAATATAGAAATGATTGAA 585

Qy 541 AATGGGTATCATCAGAGGAGCTGGGCAACTACAAACAACCAACAGCAGCAGATACCTTTT 600
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Qy 601 GCCTTCGGGTGAGCTTATTCAGCCAAATCTCCAGAGAGAGATCTA 647
Db 637 GCCCTTCGAGTTTCAGCCAAATTCAGCCAAATCTACATGAAAGAAATGTA 683

RESULT 8
PHPMDS2

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LOCUS PHPADS2 971 bp mRNA linear PLN 06-OCT-1994
DEFINITION P.hydrida mRNA for pma2s 2.
ACCESSION X69947
VERSION X69947.1 GI:22666
KEYWORDS developmental gene; DNA-binding transcription factor; MADS-box protein; pma2s 2 gene.
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 971)
Kush, A., Brunelle, A., Shevell, D. and Chua, N.H.
The cDNA sequence of two MADS box proteins in Petunia
Plant Physiol. 102 (3), 1051-1052 (1993)
94105323
MEDLINE 8278527
PUBMED
REFERENCE 2 (bases 1 to 971)
Brunelle, A.N.
Direct Submission
AUTHORS
TITLE Submitted (23-NOV-1992) A.N. Brunelle, The Rockefeller University,
JOURNAL Dept of Plant Molecular Biology, 1230 York Avenue, New York, NY
10021, USA
COMMENT The MADS transcription factor open reading frame is very similar to the GLO protein from Antirrhinum majus.
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VKLRHLGEDIINLHKLMBEGLTGLSSISAKSEILRMVRNQDILEEHKQL
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ORIGIN
Query Match 37.9%; Score 329.4; DB 8; Length 971;
Best Local Similarity 70.6%; Pred. No. 3e-72;
Matches 457; Conservative 0; Mismatches 181; Indels 9; Gaps 1;
QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGGCGAGTGACC 60
DB 45 ATGGGAGAGGAAGATAGATTAAGAGATAGAGACCTACGACAGGCGAGTTACT 104
QY 61 TACTCCAAAGAGGAGGAATGGGATATCAAGAAAGCAAGAGAGATCATCTGTTCTATGTAT 120
DB 105 TACTCCAAAGAGGAATGGGATATCAAGAAAGCTAAAGAAATCACTGTTCTTTGTAT 164
QY 121 GCTAAGTATCTCTATCATTTATCTAGCTCTGGAGAGTGTGAATCTGCGAGCCT 180
DB 165 GCTAAGGTTCCCTTATCATCTTTGGTAATTTCTGCGAGATGCGATGATTTGAGCCCT 224
QY 181 TCACTACGCTGACAGAAATCTTGGACAAATACCATGGACAAATCTGGGAAGAAGTTGTGG 240
DB 225 TCTACTAGTTACCTGATATGCTGGATGTTATCAAAAACTTCTGGAGGAGGCTATGG 284
QY 241 GATGCTAAGCATGAGAACTCAGCAATCAAGTATGATAGATCAAGAAAGCAATGACAGC 300
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QY 301 ATGCAAGTAGAGCTAGGCACTGAAGGAGAGATATCATCATTTGAACCATGTAGAG 360
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QY 361 CTGATGGCTTTAGAGGAGCACTTGAATGGCTTACAGTATCCGGGACAGCATGCC 420
DB 405 CTTATGGTTTGGAGAGGCTTAACAAATGGACTTTCTAGTATCAGTGGCAAGCATCG 464
QY 421 AAGTTCTGTCGACATGATGAGAGACAATGGAAGGCACTGGAAGATGAGAATAAGCGCTC 480
DB 465 GAGATCTTGGAGTGGTTCGAGAAATGATCAATTTCTGGAGGAGGAACACAGCAACTT 524
QY 481 ACTTATGAGCTGCAAAAACCAACAGAGATGAAATAAAGAGATGTGAGAAATGGAA 540
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QY 541 AATGGTATCATCAGAGCGAGCTGGGAACTTACAAACCAACAGGAGAGATACCTTTT 600
DB 585 GAATGTACCAATCAAGAGACAGG-----ATTACGATACAGAGATGCCATTT 635
QY 601 GCCTTCCGCTGCGCTTATTCAGCCAAATCTCCAGGAGAGAACTCTA 647
DB 636 GCCTTCGAGTTCAGCAATGCAGCAATCTACATGAAGAATGTA 682
RESULT 9
NTGLOBOSA 768 bp mRNA linear PLN 10-JUN-1993
LOCUS N.tabacum GLO mRNA.
DEFINITION X67959
ACCESSION X67959
VERSION X67959.1 GI:19870
KEYWORDS DNA binding protein; transcription factor.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 768)
Hansen, G., Estruch, J.J., Sommer, H. and Spena, A.
NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of Antirrhinum majus: cDNA sequence and expression pattern
Mol. Gen. Genet. 239 (1-2), 310-312 (1993)
93288002
MEDLINE 8099711
PUBMED
REFERENCE 2 (bases 1 to 768)
Hansen, G.
Direct Submission
AUTHORS
TITLE Submitted (03-AUG-1992) G. Hansen, Max-Planck Inst. fuer
JOURNAL Zuchtungsforshung, Carl-von-Linne Weg, 10, 5000 Koeln 30, FRG
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ORIGIN


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KEYWORDS      Petunia x hybrida
SOURCE        Petunia x hybrida
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; lamids; Solanales; Solanaceae; Petunia.
REFERENCE     1 (bases 1 to 780)
AUTHORS       Van, T.A., Mollena, C., Angenent, G.C. and Dons, J.J.
TITLE         A METHOD FOR OBTAINING A PLANT HAVING ALTERED FLORAL MORPHOLOGY AND
              A METHOD FOR PROTECTING PLANTS AGAINST PEST INSECTS
JOURNAL       Patent: WO 940582-A 1 06-JAN-1994;
              FOR PLANT BREEDING AND REPRODUCTION (NL)
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QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGCGAGTGACC 60
DB 8 ATGGGAGAGGAAAGATAGAGATAAAGAAATAGAAAATCAAGCAACAGCAAGTAACT 67
QY 61 TACTCCAGAGGAGGATGGATATCAAGAGGCAAGGAGATCACTGTTCTATGTGAT 120
DB 68 TACTCAAAAAGAGAAATGGATCTTGAAAAAGCTTAAGGAAATAGTGTCTTTGTGAT 127
QY 121 GCTAAAGTATCTCTTATCATTTTCTAGCTCTGGGAAGATGGTTGAATCTGACGCCCT 180
DB 128 GCTCGTGTCTCTGTTATCATTTTCTAGCTCTGGGAAGATGGTTGAATCTGACGCCCT 181
QY 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACCATGGACATCTGGGAAGAGTGTGG 240
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DB 242 GATGCTAAGCATGAGAACCTGGAACATGAATCAACAACTCAAGAAAGCAATGACAC 301
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DB 302 ATGCAAAATGAATCAGGCACTTGAAGGTTGAAGATATCATCATTTTGAACCATGAGAG 361
QY 361 CTGATGCGCTTAGAGGAGCACTTGAAGATGGCTTACAGATTCGGGCAAGCAGTGCC 420
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QY 421 AAGTTCGTCGATGATGAGAGCAATGGAAGGCACTGGAAGATGAGAAATGAGCGCCTC 480
DB 422 GAGGTTCTGAGGATGATGAGGAGAAAGACTCAAAAGTATGAGGAGGAGCAAGCAACTT 481
QY 481 ACTTATGAGCTGCAAAAACACAGGAGATGAAATAAAGAGATGTGAGAAACATGGAA 540

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482 AATTGCCAATTGCGCAACTTGGATAGCAACCATGAATAGGAATATGGGAGAAATTGGC 541
541 AATGGGTATCATCAGAGCGAGCTGGGAACTACAAACACACAGCAGCAGATACCTTTT 600
542 GAAGTGTTTTCAGCAGAGGAG-----AATCATGACTACCAAAACCATATGCTTTT 592
601 GCCTTCGCGTGCAGCCCTATTTCAGCCAAATCTCCAGGAGAGAATCTAATTAGATA 655
593 GCCTTCGAGTACAAACCAATGCAAGCAATTTGAGGAGAGGTTGTAATAAAGA 647

RESULT 12
PETRNSFA      780 bp  mRNA  linear  PLN 27-APR-1993
LOCUS         Petunia transcription factor (fbpl) RNA, complete cds.
DEFINITION    M91190
ACCESSION     M91190.1 GI:169253
VERSION       93005737
KEYWORDS      transcription factor.
SOURCE        Petunia x hybrida
ORGANISM      Petunia x hybrida
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; lamids; Solanales; Solanaceae; Petunia.
              1 (bases 1 to 780)
REFERENCE     Angenent, G.C., Busscher, M., Franken, J., Mol, J.N. and van Tunen, A.J.
              Differential expression of two MADS box genes in wild-type and
              mutant Petunia flowers
AUTHORS       Plant Cell 4 (8), 983-993 (1992)
TITLE         1356537
JOURNAL       PUBMED
MEDLINE       1356537
COMMENT       Original source text: Petunia hybrida (strain R27) flower petals
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ORIGIN
Query Match      33.6%;   Score 291.4;   DB 8;   Length 780;
Best Local Similarity 67.8%;   Pred. No. 1.2e-62;
Matches 444;   Conservative 0;   Mismatches 196;   Indels 15;   Gaps 2;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGCGAGTGACC 60
DB 8 ATGGGAGAGGAAAGATAGAGATAAAGAAATAGAAAATCAAGCAACAGCAAGTAACT 67
QY 61 TACTCCAGAGGAGGATGGATATCAAGAGGCAAGGAGATCACTGTTCTATGTGAT 120
DB 68 TACTCAAAAAGAGAAATGGATCTTGAAAAAGCTTAAGGAAATAGTGTCTTTGTGAT 127
QY 121 GCTAAAGTATCTCTTATCATTTTCTAGCTCTGGGAAGATGGTTGAATCTGACGCCCT 180
DB 128 GCTCGTGTCTCTGTTATCATTTTCTAGCTCTGGGAAGATGGTTGAATCTGACGCCCT 181
QY 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACCATGGACATCTGGGAAGAGTGTGG 240

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Db 182 TCTACTTCGTTGGTGTATTTTGGATCAATATACAAAGCTTACTGTGTAAGATTGTTG 241
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 Db 242 GATCCTAAGCATGAGAACCTTGGCAATGAATCAACAAAGTCAAGAAAGACAATGACAAAC 301
 Qy 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGATATACATCATGTAACCATGTAGAG 360
 Db 302 ATGCAAAATTGAATCAGGCACCTTGAAGGCTGAAGATATACATCTTTGAACCATAGAGAG 361
 Qy 361 CTGATGCGCTTAGAGGAGACACTTGAATGGCCTTACAGTATCCGGGACAGAGCTCC 420
 Db 362 CTATGATATATGGAAGATGCCCTTGAATGGACTACTAGTATTCGTACAAACAGAAAT 421
 Qy 421 AAGTTCGTCACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGAAATAGCCCTC 480
 Db 422 GAGGTTCTGAGGATGATGAGAAAGAAAGACTCAAGTATGAGGAGGCAAGACCACTT 481
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 Db 482 AATTGCCAATTGGCCCAACTTGAATAGACCAACCATGAATAGGAATATGGAGAAATTGCG 541
 Qy 541 AATGGGTATCATCAGAGCGAGCTGGGAACTACAAACCAACAGCAGCAGATACCTTTT 600
 Db 542 GAAGTGTTTTCAGCAGAGGGAG-----AATCATGACTTACCAAAACCATATGCCCTTT 592
 Qy 601 GCCTTCGCTGCGCTTATTCAGCCAAATCTCCAGAGAGAAATCAATTAGATA 655
 Db 593 GCCTTCGCGTACAAACCAATGCAGCCAAATTTTCAGGAGAGGTTGTAAAAAAGA 647

RESULT 13

AV173061
 LOCUS Chrysanthemum x morifolium MADS-box transcription factor CDM86
 DEFINITION (cdm86) mRNA, complete cds.
 ACCESSION AV173061
 VERSION AV173061.1 GI:27804368

KEYWORDS Chrysanthemum x morifolium (Dendrathera grandiflora)
 ORGANISM Chrysanthemum x morifolium

REFERENCE 1 (bases 1 to 814)
 Schennikov A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Unpublished
 TITLE Chrysanthemum MADS-box transcription factor CDM86
 JOURNAL

REFERENCE 2 (bases 1 to 814)
 Schennikov A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Direct Submission
 TITLE Submitted (05-NOV-2002) Plant Development and Reproduction. Plant
 Research International, Droeveendaalsesteeg 1, Wageningen 6700 AA,
 The Netherlands

FEATURES

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ORIGIN

Query Match 33.2%; Score 288.4; DB 8; Length 814;
 Best Local Similarity 73.7%; Pred. No. 6.7e-62;
 Matches 367; Conservative 0; Mismatches 131; Indels 0; Gaps 0;
 Qy 1 ATGGGACGTGGGAGGTTGAGATCAAGAGAGGTTGAGAACTCAAGTACAGCAGGTGACC 60
 Db 37 ATGGGACGGGAAAGATAGAGATCAAGAGGATAGAAAACACAAAGTAAACAGACAGTCA 96
 Qy 61 TACTCCAGAGGAGGAATGGGATTTATCAAGAAAGGCAAGGAGAGATCACTGTTCTATGTGAT 120
 Db 97 TATTCAAAAGAGAAAGATGGAATCATCAAGAGACTAAAGAAATAACTGTTCTTGTGAT 156
 Qy 121 GCTAAAGTATCTCTTATCATTTTATCTAGCTCTCGGGAAGATGGTTGAATATCTGAGCCCT 180
 Db 157 GCTAATGTCTCTTGTATCTATGATGCTCTTCTGGCAAGATGTATGATGATCTGAGCCCT 216
 Qy 181 TCAACTACGCTGACAGAAATCTTGGACAAATACCATGCAATCTGGGAAGAGTTGTGG 240
 Db 217 AAACATAATTGATGATGATGCTGATCATCAAGAGCTTCTGGAACAAAGTTGTGG 276
 Qy 241 GATGCTAAGCATGAGAACCTCAGCAATGAAGTGGATAGATCAAGAAAGACAATGACAGC 300
 Db 277 GATGCTAAACATGAGAAATCTTCAGAAATGAAATGATAGAAATCAAGAAAGAAATGAAAGC 336
 Qy 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCACATCATTTGACCATGTAGAG 360
 Db 337 ATGCAATAGAGCTCAGGCATCTGAAGGAGAGATATCACATCTTTGAACTATGAGAA 396
 Qy 361 CTGATGCGCTTAGAGGAGCACTTTGAAAATGGCCTTACAAAGTATCCGGGCAAGCAGTCC 420
 Db 397 CTAATTCGTATGAAGATGCATTTGAAAATGGACTCAACCAATATCCGTGAGAAAAAGAT 456
 Qy 421 AAGTTCGTCACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATGAGATGAGCCCTC 480
 Db 457 GACATCCCCAAAATCATGAGAAAGATGAGCAAGTTTGGAGGAGGAAAAATAGCATCTT 516
 Qy 481 ACTTATGAGCTGCAAAAA 498
 Db 517 ATGATATTAGTGCAACA 534

RESULT 14

AF029976
 LOCUS Eucalyptus grandis MADS box protein (EGM2) mRNA, complete cds.
 DEFINITION AF029976
 ACCESSION AF029976
 VERSION AF029976.1 GI:3114585
 KEYWORDS Eucalyptus grandis
 SOURCE Eucalyptus grandis

ORGANISM Eucalyptus grandis

REFERENCE 1 (bases 1 to 920)
 Southern, S.G., Marshall, H., Mouradov, A. and Teasdale, R.D.
 Eucalypt MADS-box genes expressed in developing flowers
 Plant Physiol. 118 (2), 365-372 (1998)

REFERENCE 2 (bases 1 to 920)
 Southern, S.G., Marshall, H.O. and Teasdale, R.D.
 Direct Submission

REFERENCE 3 (bases 1 to 920)
 Southern, S.G., Marshall, H., Mouradov, A. and Teasdale, R.D.
 Eucalypt MADS-box genes expressed in developing flowers
 Plant Physiol. 118 (2), 365-372 (1998)

REFERENCE 4 (bases 1 to 920)
 Southern, S.G., Marshall, H.O. and Teasdale, R.D.
 Direct Submission

REFERENCE 5 (bases 1 to 920)
 Southern, S.G., Marshall, H., Mouradov, A. and Teasdale, R.D.
 Eucalypt MADS-box genes expressed in developing flowers
 Plant Physiol. 118 (2), 365-372 (1998)

REFERENCE 6 (bases 1 to 920)
 Southern, S.G., Marshall, H., Mouradov, A. and Teasdale, R.D.
 Eucalypt MADS-box genes expressed in developing flowers
 Plant Physiol. 118 (2), 365-372 (1998)

FEATURES

source
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/db_xref="taxon:71139"
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ORIGIN
Query Match 32.3%; Score 280.2; DB 8; Length 920;
Best Local Similarity 69.3%; Pred. No. 7.9e-60;
Matches 397; Conservative 0; Mismatches 173; Indels 3; Gaps 1;

Qy 1 ATGGGAGCTGGGAAGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGCGCAGGTGACC 60
Db 53 ATGGGAGAGGGAAGATAGAGATAAGAGGATAGAGAACTCAACACAGGCAAGTTACC 112
Qy 61 TACTCCAGAGGAGGAATGGGATTCACAGAGGCAAGAGGATCACTGTTCTATGTGAT 120
Db 113 TACTCCAGAGGAGGAACGGGCTCATCAAGAGGCAAGAGGATTCCTGTTCTGTGTGAT 172
Qy 121 GCTAAAGTATCTTATCATTTATCTTAGCTCTGGGAAGATGTTGAAATCTCGACCCCT 180
Db 173 GCTCAAGTCTCTGTGATCATCTTTGGTAGCTCCGGGAGATGATGATGATGATGATGAT 232
Qy 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACATGGCAATCTCGGAAGAAAGTTGTGG 240
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Qy 241 GATGCTAAGCATGAGACCTCAGCAATGAGTGGATAGTCTCAAGAGACATGACAGTACAGC 300
Db 293 GATGCTAAGCAAGAAATCTGAGCAATGAACTAGATAGGATCAAAAGAGGAAACGCAAC 352
Qy 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
Db 353 TTGCAGATTTCAGCTCAGCCACCTGAAAGGAGAGACATAACATCACTGAACCAACAGAG 412
Qy 361 CTGATGCCCTTAGGAGAACCTTGAATGGCTTACAAAGTATCCGGNACAGCAGTCC 420
Db 413 CTGATAATCTTAGAAGACATCTTTGAAAACGGCGTCGGATGTGTCCGAGACCAAGAGGAC 472
Qy 421 AAGTTCTGCACATGATGAGAGCAATGGAAAGGCACTGGAAGATGAGATAAGCGCCTC 480
Db 473 GAAGTTCTGATGACGACAGAGGAATCAAGACAGCTGGAGGAGCGCTAAGAGCTC 532
Qy 481 ACTTATGAGCTGCAAAACACAGGAGATGAAATAAAGAGAAATGTGAAACATGGA 540
Db 533 CATTTCTATGGCC---AACAAAAGACATGATGATGCGCGAAATCTGTAGAGCTGGGAAC 589
Qy 541 AATGGGTATCATCAGAGCAGCTGGGAACCTAC 573
Db 590 GACGGTTACCATCAAGAAATGAAGGCTGACTTC 622

RESULT 15
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LOCUS AB079259 807 bp mRNA linear PLN 02-APR-2003
DEFINITION Agapanthus praecox ApMADS1 mRNA for MADS-box transcription factor
PI, complete cds.
ACCESSION AB079259
VERSION AB079259.1 GI:29467045
KEYWORDS Agapanthus praecox
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Agapanthus praecox
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Agapanthaceae; Agapanthus.
1
Nakamura,T. and Nakano,M.
The MADS-box gene which expressed in floral organs of Agapanthus
praecox
Published Only in Database (2003)
2 (bases 1 to 807)
Nakamura,T. and Nakano,M.
Direct Submission
Submitted (02-FEB-2002) Toru Nakamura, Niigata University, Fac. of
Agriculture; 2-8050 Ikarashi, Niigata, Niigata 950-2181, Japan
(E-mail: f01e402@mail.cc.niigata-u.ac.jp, Tel:81-25-262-6598,
Fax:81-25-262-6858)
Location/Qualifiers
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/codon_start=1
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/db_xref="GI:2946704"
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IELRHLKEDLNSLPKELIPIEALENGSLVRAKOMEYLMKLNKLERLLEENKRL
TYILHQQLAMEGNVRQLDLYGHQREPERFAQMPAFRVQPIHPLQNNK"

ORIGIN
Query Match 32.1%; Score 278.8; DB 8; Length 807;
Best Local Similarity 64.1%; Pred. No. 1.8e-59;
Matches 459; Conservative 0; Mismatches 242; Indels 15; Gaps 2;

Qy 1 ATGGGACGTGGGAAGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGCGCAGGTGACC 60
Db 41 ATGGGGCCAGGAAAGATCGAGATCAAGCGGATCGAGAAATCGACAAACCGGAGCTACT 100
Qy 61 TACTCCAGAGGAGGAATGGGATTCACAGAGGCAAGAGGATCACTGTTCTATGTGAT 120
Db 101 TTCTCGAAGCGCGGAATGGCATCATCAAGAAAGCTAGAGAGATCAGCGTCTTTTGGCAA 160
Qy 121 GCTAAAGTATCTTATCATTTATCTTAGCTCTGGGAAGATGTTGAAATCTCGACCCCT 180
Db 161 TCACAAGTCTCTGTTGTGATCTTCTAGCTGTGGGAAGATGTCGTGATTTGCGACCA 220
Qy 181 TCAACTACGCTGACAGAAATCTTGACAAATACCAATGGCAATCTGGGAAGAAAGTTGTGG 240
Db 221 AACACTCTGTTCCGAGGATTTGGAGAGGTACACAGCAACTGTGGGAAGAGCTATGG 280
Qy 241 GATGCTAAGCATGAGAACTCAGCAATGAAGTGGATAGAGTCAAGAAAGACATGACAGC 300
Db 281 GATGCTAAGCATGAGAACTTAAATGCCAGATCGATCGGGTTAAGAAAGAGATGATGATAC 340
Qy 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCACATCATTTGAACCATGTAGAG 360
Db 341 ATGCAAAATGAGCTCAGGCATTTGAAGGGAGGATTTGAATCTCTGAAATCAAGGAA 400
Qy 361 CTGATGGCCTTAGAGAAAGCACTTGAAAATGSCCTTACAAGTATCCGGGCAAGCAGTCC 420
Db 401 CTGATACCGATCGAAGAGCTCTCGAAGACGAGCTCAATGGTGTCCGAGCTAAGCAGATG 460
Qy 421 AAGTTCTGACATGATGAGAGACATGGAAGGCACTGGAGATGAGATGAGATAAGCGCTC 480
Db 461 GAATACTTGAGATGTTGAAAAGAAATGAAAGGCTTCTGGAAAGAGGAAATTAAGAGATTG 520
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Qy 481 ACTTATGAGCTGCAAAACACAGGAGATGAAATAAAGAGAAATGTGAGAAACATGGAA 540
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Db 521 ACTTATATCCTGC---GCCATCAGCAATTGGCGATGGAGGAAATGTGAGGCAATTGGAT 577
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Qy 541 AATGGGTATCATCAGAGCGAGCTGGGGAACCTACAACAAACCCAGCAGCAGATACCTTTT 600
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Db 578 CTCGGATATCACCAGAGAGAAAGGG-----AGTTTGGCGCGCAGATGCCAATG 625
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Qy 601 GCCTTCGCGGTGCGAGCCTATTTCAGCCAAATCTCCAGGAGAGATCTAAATTAGATATCT 660
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Db 626 GCCTTCGCGGTGCGAGCCTATCCACCAAAATTACAGCAGAACAAATATGATCAAAAC 685
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Qy 661 TGCATTTGCATGCTCTTTTAACTAGTATATATCTCTCCACCTCTCTCTCTTT 716
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Db 686 AATCATTTTGTGCGCCCGCTATCTTTATATTCGTATATATCTTGTATCTTACCT 741
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Search completed: September 25, 2004, 18:20:15
Job time : 3670.24 secs

APPLICANT: BERNALDO NAQAI-GINALD
TITLE OF INVENTION: MYOCYTE-SPECIFIC

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; TITLE OF INVENTION: TRANSCRIPTION
; TITLE OF INVENTION: ENHANCING FACTOR 2
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US93-08386-15

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Query Match 28.3%; Score 344; DB 5; Length 84;
Best Local Similarity 74.7%; Pred. No. 1.4e-26;
Matches 62; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 3 RGKIEIKLIENQTNROVTSYKERNIGFKKAOELTVLCDARVSLMLNTNOMHEYISPTT 62
Db 1 RGKIQIKRIENQTNROVTSYKERNIGFKKAOELTVLCDARVSLMLNTNOMHEYISPTT 60

QY 63 TTKSMYDDYQKTMGIDLWRTHEE 85
Db 61 ATKQLFDYQKAVGVDLWSSHYE 83

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RESULT 3
PCT-US93-08386-14
; Sequence 14, Application PC/TUS9308386
; GENERAL INFORMATION:
; APPLICANT: Bernardo Nadal-Ginard
; TITLE OF INVENTION: MYOCYTE-SPECIFIC
; TITLE OF INVENTION: TRANSCRIPTION
; TITLE OF INVENTION: ENHANCING FACTOR 2
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US93-08386-14

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Query Match 25.8%; Score 314; DB 5; Length 84;
Best Local Similarity 70.7%; Pred. No. 1.3e-23;
Matches 58; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 4 GKIEIKLIENQTNROVTSYKERNIGFKKAOELTVLCDARVSLMLNTNOMHEYISPTT 63
Db 2 GKIEIKLIENQTNROVTSYKERNIGFKKAOELTVLCDARVSLMLNTNOMHEYISPTT 61

QY 64 TTKSMYDDYQKTMGIDLWRTHEE 85
Db 62 TTKMIDYQKALGVDLWSSHYE 83

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RESULT 4
PCT-US93-08386-16
; Sequence 16, Application PC/TUS9308386
; GENERAL INFORMATION:
; APPLICANT: Bernardo Nadal-Ginard
; TITLE OF INVENTION: MYOCYTE-SPECIFIC
; TITLE OF INVENTION: TRANSCRIPTION
; TITLE OF INVENTION: ENHANCING FACTOR 2
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:

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LENGTH: 84
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-08386-16

Query Match 25.7%; Score 313; DB 5; Length 84;
Best Local Similarity 71.1%; Pred. No. 1.6e-23;
Matches 59; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 3 RGKIEIKLIENQTNROVTVSKRRNGIFKKAQELTVLDCDAKVSILMLSNKMKHEIYISPTT 62
DB 1 RGKIQIKRIENQTNROVTVSKRRNGIFKKAQELTVLDCDAKVSILMLSNKMKHEIYISPTT 60

QY 63 TTKSMYDDYOKTGMGIDLWRTHES 85
DB 61 TTKEIVDLVQITISDVVDVATQYE 83

RESULT 5
US-08-867-087B-15
; Sequence 15, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan, E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-15

Query Match 24.3%; Score 295; DB 2; Length 249;
Best Local Similarity 33.1%; Pred. No. 4.2e-21;
Matches 83; Conservative 41; Mismatches 71; Indels 56; Gaps 9;

QY 1 MARGKIEIKLIENQTNROVTVSKRRNGIFKKAQELTVLDCDAKVSILMLSNKMKHEIYISPTT 60
DB 1 MGRGRVELKRIENKINRQVTFKRRNGLLKAYELSVLDCDAEVALIIFSRNKGKLYEFCST 60

QY 61 TTTTSMYDDYOKT--MGIDLWRTHES-----MKDTLWKLKEINNKLRREIRORLGHDL 113
DB 61 QSMTKTL-ETQKCSYAGPETAQVQRESEQLKASRNEYLKARVENLQRTQRLNLLGPD 119

QY 114 NGLSPDELASLDDEMOSSLDAIR-----ORKYHVIKTQTETTTKKVKVLEQ 159

DB 120 DSLGKTELESLEKQLDSSLKHVTRTRTKHLVDLTLOKQKQMYSEANRCLRKLSESNH 179

QY 160 REGNN-----LHG-----YFQDEAAGBDP-QYGY--EDNEDGYESA 192

DB 180 VRGQQVWEQGCNLCIGYERQPEVQQLHGGNGFFHPLDAAAGEPTLQIGYPAEHHE----- 233

QY 193 LALSNGANNLY 203
DB 234 -AMNSACMNTY 243

RESULT 6
US-08-867-087B-11
; Sequence 11, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan, E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-11

Query Match 23.8%; Score 290; DB 2; Length 241;
Best Local Similarity 36.7%; Pred. No. 1.2e-20;
Matches 77; Conservative 34; Mismatches 69; Indels 30; Gaps 6;

QY 1 MARGKIEIKLIENQTNROVTVSKRRNGIFKKAQELTVLDCDAKVSILMLSNKMKHEIYISPTT 60
DB 1 MGRGRVELKRIENKINRQVTFKRRNGLLKAYELSVLDCDAEVALIIFSRNKGKLYEFCSS 60

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QY 61 TTTTSMYDDYOK-----TWGIDLWTHESKMDTLWLKLEINNKLRREIRQRGLHDIN 114
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QY 115 GLSPFELASLDDEMQSSLDAIR-----QRKYHVIKTQETTKKKVKNLEQR 160
DB 120 PUNSKESLESRLQDMSLKQIRSTRQMLDQULTDLQRKEHALNEANRLKQRL-----M 174
QY 161 RGNMLHYFDQEAAGEDPQYGYE--DNEG 188
DB 175 EESQLNLQWQONA--QDMGYGROTTOTQGD 202

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RESULT 7
US-08-867-087B-17
; Sequence 17, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204

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COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35, 123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
US-08-867-087B-17

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Query Match      23.6%; Score 287; DB 2; Length 248;
Best Local Similarity 37.7%; Pred. No. 2.5e-20;
Matches         75; Conservative 35; Mismatches 69; Indels 20; Gaps 6;

YY 1 MARGKLEIKLIENQTNRQVITYSKRNGIFPKKAQLTVLCDAKVSLIMLSNTNRKHVEYISP 60
bb |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
1 MGRGRVELKRRIENKNRQVTFAKRENGLLKKAYELSVLCDAEVALIIFSNRGKLYEPCSG 60

YY 61 TTTTYSMDYDYOKTW--GIDLWRTHEE-----SWKDITLWLKEINNKLRREIQRLGHDL 113
bb |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
61 QSWTRTL-ERYOKFSYGGPDAIQNKEVLQVGSNEYVKLKARVENLQRTQRNLAGEDL 119

YY 114 NGLSFEDELASLDDEMQSSLDAIRO-RKYHVIAKTQTETTKKVKNLEORR-----GNM 164

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Db      120 GTLGIKLEQLKQDSSLRIHSTRTQWMLDQLTQRREQMCEANKCLRKLEESNQ 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      165 LHGYFDQEAAGEDPQGYE 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      180 LHGQWEHGA---TLGYE 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 8
US-09-611-659A-4
; Sequence 4, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Mac, Long
; APPLICANT: Rod, Wing
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611,659A
; CURRENT FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-611-659A-4

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[illegible]

US-09-067-800-2
 Sequence 2, Application US/09067800
 Patent No. 6198024
 GENERAL INFORMATION:
 APPLICANT: Yanofsky, Martin F.
 APPLICANT: Ferrandiz, Cristina
 TITLE OF INVENTION: Seed Plants Characterized by Delayed
 TITLE OF INVENTION: Seed Dispersal
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: United States
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/067,800
 FILING DATE:

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-800-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTVSKRRNGIFPKKAQELTVLCAKVSLLMLSNNTKMHYISP 60
DB 1 MGRGRVQLKRIENKINRQVTFKRRSGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY-----QKTWGDIDLRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSLSDAIRQKYHVTKQTETTTKKVKVNLQRRGNMLHGYF 169
DB 114 GEDLDSLSLKELQSLHQLDAIRKQYVTSRSDGFRVGVGGGASSLT-----EPN 227
QY 170 DOE-AAGED-----POGYEDNEGDIYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFRVGVGGGASSLT-----EPN 227

RESULT 10
US-09-105-652-2
; Sequence 2, Application US/09105652
; Patent No. 6229068
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin P.
; APPLICANT: Martienssen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/105,652
; CURRENT FILING DATE: 1998-06-26
; EARLIER APPLICATION NUMBER: 60/051,030
; EARLIER FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-105-652-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTVSKRRNGIFPKKAQELTVLCAKVSLLMLSNNTKMHYISP 60
DB 1 MGRGRVQLKRIENKINRQVTFKRRSGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY-----QKTWGDIDLRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSLSDAIRQKYHVTKQTETTTKKVKVNLQRRGNMLHGYF 169

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DB 114 GEDLDSLSLKELQSLHQLDAIRKQYVTSRSDGFRVGVGGGASSLT-----EPN 227
QY 170 DOE-AAGED-----POGYEDNEGDIYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFRVGVGGGASSLT-----EPN 227

RESULT 11
US-09-349-677-2
; Sequence 2, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin P.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-349-677-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTVSKRRNGIFPKKAQELTVLCAKVSLLMLSNNTKMHYISP 60
DB 1 MGRGRVQLKRIENKINRQVTFKRRSGLLKAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY-----QKTWGDIDLRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSLSDAIRQKYHVTKQTETTTKKVKVNLQRRGNMLHGYF 169
DB 114 GEDLDSLSLKELQSLHQLDAIRKQYVTSRSDGFRVGVGGGASSLT-----EPN 227
QY 170 DOE-AAGED-----POGYEDNEGDIYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFRVGVGGGASSLT-----EPN 227

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RESULT 12
US-09-708-584-2
Sequence 2, Application US/09708584
Patent No. 6541683
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Martienssen, Robert
APPLICANT: Ferrandiz, Cristina
APPLICANT: Gu, Qing
TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
FILE REFERENCE: P-UD 3040
CURRENT APPLICATION NUMBER: US/09/708,584
CURRENT FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: 09/105,652
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/051,030
PRIOR FILING DATE: 1997-06-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-708-584-2

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Query Match      23.0%; Score 280; DB 4; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY      1  MARGKIEIKLENTNQVTSKRRNGIPKQACELTVLCAKVLMLSNNTKQHEIYSP 60
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1  MGRGEVQLKRLINKINQVTSKRSGLLKKAEHSVLCAEAVLIVSSGKGFPEIYSD 60

QY      61  TTTTKSM--YDY-----QKTWGIDLNRTHESMKDTLWLKLEINNKLRREI----RQRL 109
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      61  SCMERILERYDRLYSDQLQVGRDVSQSEN-----WVLEHAKLKARVEVLEKNKRNFM 113

QY      110  GHDLNGLSFDELAISDDMOSSLDATQRKYHVIKTQTETTKKVKVKNLEQRRGNWLHCYF 169
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      114  GEDLDLSLKLQSLQHLDPAIKSIRSRKNQAMFESISALQKKDKALQDNNSLLKKIK 173

QY      170  DOE-AAGED-----POGYVEDNGDYESALALNSGANNLYTFHLHPN 211
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      174  EREKTKQGBQLVQCNSNSVLLPYCVTSRDRGFVERVGGENGASSLT-----EN 227

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RESULT 13
US-09-067-800-8
; Sequence 8, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandi, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-800-8

Query Match      22.9%; Score 279; DB 3; Length 246;
Best Local Similarity 30.6%; Pred. No. 1.5e-19;
Matches 74; Conservative 40; Mismatches 72; Indels 56; Gaps 6;

QY 1 MARGKIEIKLTENQTRNQVTSKRRNGIFKKAQELTVLCDAKVSLMLSNNTKMHY--- 57
Db 16 IGRGKIEIKRIENTNQNQVTFCKRNLGLKKAYELSVLCDAEVALVIFSTRGLRYEYANN 75
QY 58 -----ISPPTTKSYDYDYQKTMGIDLWRTHESMKDTLWKLKEINNK 101
Db 76 SVRGTIERYKACSDAVNPPTTEANTQYQBEA-----SKL 112
QY 102 RREI-----RQLRGDLNGLSFDLSDLDDEMQSSLDATRQKYHVIKQTETTKKV 154
Db 113 RQRIIDQNLRHILGESLGNFKELKNLESRLSGISRVRSKCHEMLVAEITYMOK-- 170
QY 155 KNLQRGNLHGYFDOEAAGEDPQYGYEDNEG-DYESALALSNGA-----NNLYTFPLHH 209
Db 171 REIELQNDNMYLRSKITERGLQQQSSSVIHQGYESGVTSSSHQSGQYNNRYIAVLL 230
QY 210 PN 211
Db 231 PN 232

RESULT 14
US-09-349-677-8
; Sequence 8, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:

```


TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-349-677-8
Query Match 22.9%; Score 279; DB 3; Length 246;
Best Local Similarity 30.6%; Pred. No. 1.5e-19;
Matches 74; Conservative 40; Mismatches 72; Indels 56; Gaps 6;
QY 1 MARGKIEIKLIENQTNROVTSKRRNGIFKKAQELTVLCDKAVSLMLSLNTNKHHEY--- 57
Db 16 IGRGKIEIKRIENTTNROVTFCKRNGLLKKAELSVLCDAEVALVIFSTRGRLEYANN 75
QY 58 -----ISPTTTKSMYDDYQKTMGIDLWRTHESMDTLWLKKEINNKL 101
Db 76 SVRGTIERYKKACSDAVNPFTITANTQYQEA-----SKL 112
QY 102 RREI-----RQRGLHDLNGLSFDLASLDDMOSSLDALRQRYHVIKTQTETTKKV 154
Db 113 RQRIQDQNLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQ-- 170
QY 155 KNLQRRGNMLHGYDQEAAGEDPOGYVEDNEG-YESALALSNGA-----NNLYTEHLH 209
Db 171 REIELQNDNMYLRSKITERTGLQQQESSVIHQGTYESGVTSQSGQYNNYIANVLE 230
QY 210 PN 211
Db 231 PN 232

RESULT 15
US-08-904-284-7
Sequence 7, Application US/08904284
Patent No. 6133435
GENERAL INFORMATION:
APPLICANT: Fernandez, Donna E.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
TITLE OF INVENTION: TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Finckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,284
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-904-284-7
Query Match 22.7%; Score 276; DB 3; Length 268;
Best Local Similarity 40.0%; Pred. No. 3.4e-19;
Matches 68; Conservative 33; Mismatches 41; Indels 28; Gaps 5;
QY 1 MARGKIEIKLIENQTNROVTSKRRNGIFKKAQELTVLCDKAVSLMLSLNTNKHHEYISP 60
Db 1 MGRGKIEIKRIENANSRQVTFKRRSGLLKARELSVLCDAEVAVIVFSKGLFEYST 60
QY 61 -TTTTKSMYDDYQKTMG-----IDLWRTHESMDTLWLKKEINNKLRREIRQLG 110
Db 61 GMKQTLRSRYGNHQSASSAKAEEDCAEVDI-----LKDQLSKLQEKHLQLQ-----G 106
QY 111 HDLNGLSFDLASLDDMOSSLDALRQRYHVIKTQTETTKKVKNLEOR 160
Db 107 KGLNPLTFKELQSLQQLYHALITVRERKERLLTNQLBESRLK-----EOR 152
Search completed: September 27, 2004, 09:30:03
Job time : 24.8747 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 27, 2004, 09:22:14 ; Search time 22.1253 Seconds
(without alignments)
501.670 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103

Sequence: 1 MGRGKVEIKRNSNQVT.....QQIPFAFRVQPIQPNLQERI 215

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Match Length	DB ID	Description
		Match	Length			
1	358	32.5	227	4	US-09-410-464-4	Sequence 4, Appli
2	346	31.4	273	2	US-08-592-214A-8	Sequence 8, Appli
3	346	31.4	273	3	US-08-659-188-8	Sequence 8, Appli
4	346	31.4	273	3	US-08-655-227-8	Sequence 8, Appli
5	346	31.4	273	3	US-08-655-241-8	Sequence 8, Appli
6	346	31.4	273	3	US-09-149-976-8	Sequence 8, Appli
7	346	31.4	273	4	US-09-398-326-8	Sequence 8, Appli
8	334	30.3	265	4	US-09-611-659A-4	Sequence 4, Appli
9	330	29.9	242	3	US-09-067-800-2	Sequence 2, Appli
10	330	29.9	242	3	US-09-105-652-2	Sequence 2, Appli
11	330	29.9	242	3	US-09-349-677-2	Sequence 2, Appli
12	330	29.9	242	4	US-09-708-584-2	Sequence 2, Appli
13	321	29.1	255	2	US-08-592-214A-10	Sequence 10, Appl
14	321	29.1	255	3	US-08-659-188-10	Sequence 10, Appl
15	321	29.1	255	3	US-08-655-227-10	Sequence 10, Appl
16	321	29.1	255	3	US-08-655-241-10	Sequence 10, Appl
17	321	29.1	255	3	US-09-149-976-10	Sequence 10, Appl
18	321	29.1	255	4	US-09-398-326-10	Sequence 10, Appl
19	320.5	29.1	248	3	US-09-067-800-6	Sequence 6, Appli
20	320.5	29.1	248	3	US-09-349-677-6	Sequence 6, Appli
21	319.5	29.0	246	3	US-09-067-800-8	Sequence 8, Appli
22	319.5	29.0	246	3	US-09-349-677-8	Sequence 8, Appli
23	319	28.9	252	1	US-08-450-512-5	Sequence 5, Appli
24	319	28.9	252	2	US-08-592-214A-6	Sequence 6, Appli
25	319	28.9	255	3	US-08-659-188-6	Sequence 6, Appli
26	319	28.9	255	3	US-08-655-227-6	Sequence 6, Appli
27	319	28.9	255	3	US-08-655-241-6	Sequence 6, Appli

28	319	28.9	255	3	US-09-149-976-6	Sequence 6, Appli
29	319	28.9	255	4	US-09-398-326-6	Sequence 6, Appli
30	319	28.9	285	1	US-08-460-512-2	Sequence 2, Appli
31	318	28.8	253	2	US-08-592-214A-4	Sequence 4, Appli
32	318	28.8	253	3	US-08-659-188-4	Sequence 4, Appli
33	318	28.8	253	3	US-08-655-227-4	Sequence 4, Appli
34	318	28.8	253	3	US-08-655-241-4	Sequence 4, Appli
35	318	28.8	253	3	US-09-149-976-4	Sequence 4, Appli
36	318	28.8	253	4	US-09-398-326-4	Sequence 4, Appli
37	318	28.8	255	2	US-08-576-156-2	Sequence 2, Appli
38	318	28.8	255	3	US-08-653-188-2	Sequence 2, Appli
39	318	28.8	256	3	US-08-655-227-2	Sequence 2, Appli
40	318	28.8	256	3	US-08-655-241-2	Sequence 2, Appli
41	318	28.8	256	4	US-09-398-326-2	Sequence 2, Appli
42	318	28.8	300	2	US-08-592-214A-2	Sequence 2, Appli
43	318	28.8	300	3	US-09-149-976-2	Sequence 2, Appli
44	315.5	28.6	241	2	US-08-867-087B-11	Sequence 11, Appl
45	314.5	28.5	251	2	US-08-592-214A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-410-464-4

; Sequence 4, Application US/09410464

; Patent No. 6395892

; GENERAL INFORMATION:

; APPLICANT: Strauss et al.

; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in poplar and other plant species.

; FILE REFERENCE: 53375

; CURRENT APPLICATION NUMBER: US/09/410,464

; CURRENT FILING DATE: 1999-10-01

; EARLIER APPLICATION NUMBER: 09/287,700

; EARLIER FILING DATE: 1999-04-06

; EARLIER APPLICATION NUMBER: 60/080,851

; EARLIER FILING DATE: 1998-04-06

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 4

; LENGTH: 227

; TYPE: PRT

; ORGANISM: Populus balsamifera subsp. trichocarpa

; US-09-410-464-4

Query Match 32.5%; Score 358; DB 4; Length 227;
Best Local Similarity 35.6%; Pred. No. 3.9e-26;
Matches 79; Conservative 39; Mismatches 64; Indels 40; Gaps 3;

QY 1 MGRGKVEIKRNSNQVTYKRRNGIITKAKETVLCDKAVSLIYSSSGMVEYCSP 60

Db 1 MGRGKIEIKKIENPTNRQVTSKRRNGIFKGAQELIVLCAKSLIMFNTKLNVEYISF 60

QY 61 STLTLEILDKYHQSCKLWDKAKHNLSEVDRVKDNDMSQVELRHLKGEDITSLNHVE 120

Db 61 STSTKKIYDQYQNALGIDLWGTVQYKQWHLRKLKLDINHKLQRIQRGRGGLNLSIDH 120

QY 121 LMALEALENGLTSIRDKSKFVDMWRDNGKALEDENKELTYELQKQEKIKENVRNME 180

Db 121 LRLEQHQHTALNGVGRK-----YHVIKTQNETRRKVKVNLKLE 158

QY 181 NGV-----HORQLGNVNN-----NOQIQFFAFRV 204

Db 159 ERHGNLLMEYEAKLEDQYGLVDNEAAVALANGASNLVAFRL 200

RESULT 2

US-08-592-214A-8

; Sequence 8, Application US/08592214A

; Patent No. 5811536

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

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Query Match      31.4%; Score 346; DB 3; Length 273;
Best Local Similarity 36.7%; Pred. NO. 6.9e-25;
Matches 83; Conservative 51; Mismatches 58; Indels 34; Gaps 7;

Qy      1  MGRGVEIKRIENSRNQVITYSKRRNGIIKKAETVLCDARVLIISYSSGKMWVEYCSP 60
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1  MGRGVQLKRIENKINQVITFSKRRNGLLKKAHISVLDAEVAVIVFSPGKLYEATD 60

Qy      61  STTITLILDKY--HGQSGKLMQAKHE--NLSNEVDVRKKNDSQWVLEPHLKGEDITS 115
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  SNNYITLTPYEVKVAAYVLCISFSGKQVCHVETVYKATIE--QVTVHLMQWVLEPH 110
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QY 116 LNHVELMALEALENGLTSTIRDKOS-----KFVDMRDNKALEDENKRLTYEL----- 164
Db 120 LNPKELOOLEQLODSSLKHHSRRKSHLMAESSISELOKCKERSLQEENKALOKELASRQAV 179
QY 165 ---QKQQEMKI-----KENVRNMENGYHQQLGNVYNNQQIIP 199
Db 180 ASRQOQQOQQQVQWDOQTAAQASSTSSSSPFMEQ-----DQOGLP 219

RESULT 4
US-08-655-227-8
; Sequence 8, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APSTALAL Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700

```

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:

Query Match

Db 61 S-RMDKILERYERYSAEKALISAESSEGNWCHYEYRKLKAKIETIQCKHKLWGEDLES 119
QY 116 LNHVELMALEALENGLTSTDKQS-----KFVDMRDNGKALDENKRLTYEL----- 164
Db 120 LNPKELOEQEQLDSSSLKHSRKSRLMAESISELQKRSLOENKALQKELAERQKAV 179
QY 165 ---KQOQEMKI-----KENVRNMENGYHQRLGNYNNOQOIP 199
Db 180 ASRQOQOQOQVQWQDQTHAQATSSSSSFFMRQ-----DQOGLP 219

RESULT 7
US-09-398-326-8
; Sequence 8, Application US/09398326
; Patent No. 6355863
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,326
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/659,188
; FILING DATE: 05-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-398-326-8

Query Match 31.4%; Score 346; DB 4; Length 273;
Best Local Similarity 36.7%; Pred. No. 6.9e-25;
Matches 83; Conservative 51; Mismatches 58; Indels 34; Gaps 7;

QY 1 MGRGKVEIKRIENSNRQVTYSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKMYEYCSP 60
Db 1 MGRGKVLKRIENKINRQVTFSKRRGLLKKAHEISVLCDAEAVIVFSPKGLKYEYATD 60
QY 61 STTLTEILDY--HGOSGKGLWDKHE---NLSNEVDYKNDNSMQVLRHLKGEDITS 115
Db 61 S-RMDKILERYERYSAEKALISAESSEGNWCHYEYRKLKAKIETIQCKHKLWGEDLES 119
QY 116 LNHVELMALEALENGLTSTDKQS-----KFVDMRDNGKALDENKRLTYEL----- 164
Db 120 LNPKELOEQEQLDSSSLKHSRKSRLMAESISELQKRSLOENKALQKELAERQKAV 179
QY 165 ---KQOQEMKI-----KENVRNMENGYHQRLGNYNNOQOIP 199
Db 180 ASRQOQOQOQVQWQDQTHAQATSSSSSFFMRQ-----DQOGLP 219

RESULT 8
US-09-611-659A-4
; Sequence 4, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Mao, Long
; APPLICANT: Rod, Wing
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611.659A
; CURRENT FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-611-659A-4

Query Match 30.3%; Score 334; DB 4; Length 265;
Best Local Similarity 38.1%; Pred. No. 9e-24;
Matches 82; Conservative 45; Mismatches 58; Indels 30; Gaps 8;

QY 1 MGRGKVEIKRIENSNRQVTYSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKMYEYCSP 60
Db 1 MAREKIQIKKIDNSTARQVTFKRRGLFKKABELSVLCDAVALIIFSTGKLFYSSS 60
QY 61 STTLTEILDY--YHGOSGKGLWDKHE---SNEVDYKNDNSMQVLRHLKGEDIT 114
Db 61 S--MKQILERRDLHSHKNLEK--DQPSLEQLQVENSYSRLSKSEKSHRLQRGEEQL 117
QY 115 LNHVELMALEALENGLTST---RDQSKFVDMRDNGKALDENKRLTYELQKQEM 170
Db 118 GLNTEELQQLERSLETGLSRVIERKDKIMREINQLQCKGHLWYENEKL-----RQOVM 172
QY 171 KIKENVRNMENGYHQRLG-----NYYNNQ 195
Db 173 EISNNNNNNNGY--REAGVIFEPENGFNNNNE 205

RESULT 9
US-09-067-800-2
; Sequence 2, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:

Query Match	29.9%;	Score 330;	DB 3;	Length 242;	
Best Local Similarity	35.9%;	Pred. No. 1.9e-23;			
Matches	83;	Conservative 46;	Mismatches 68;	Indels 34;	Gaps 7;
Qy	1	MGRGKVEIKRTENSSNRQVTSKERNGIIKKAKEITVLCDKAKSLIIYSSSGKQVVEYCSP	60		
Db	1	MGRGVQKRLKINRQVTSKRSGLLKKAHEISVLCDAEVALIYSSGKGLFEY-ST	59		
Qy	61	STTLTEILDKY--HQGSKKL-----WDAKHENLSNEVDRVKDNDMSQVLEAHL	108		
Db	60	DSCMERILERYDRVLYSKQLVGRDVSQSENVWLEHAKLKARVEVLEK-----RNF	112		
Qy	109	KGEITSLNHVELMALEALNGTISIRDKOS---KFDVMRDNGKALEDENKELTYEL	164		
Db	113	MGEIDLDSLSLKELOSLQHLPDAIKSIKRNQAMFESISALOKDKALQDHNSLL----	169		
Qy	165	QKQEMKIKENVRNMENYHQRQLGNYNVNNQQIIPFAFRVQFIQPNLOERI	215		
Db	170	-----KTKKE---REKKTGOEGOLVCCSNSSSVLLPQYCVTSSRRDGFVERV	213		

RESULT 12
US-09-708-584-2
; Sequence 2, Application US/09708584
; Patent No. 6541683
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.

```

; APPLICANT: Martienssen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/708,584
; CURRENT FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 05/105,652
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/051,030
; PRIOR FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; US-09-708-584-2

Query Match          29.9%; Score 330; DB 4; Length 242;
Best Local Similarity 35.9%; Pred. No. 1.9e-23;
Matches 83; Conservative 46; Mismatches 68; Indels 34; Gaps 7;

Qy 1 MGRGKVEIKRIENSSNRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQVYCSF 60
Db 1 MGRGVQLKRIENKINRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQVYCSF 59
Qy 61 STTLTEILDKYHQS---GKGLWDKDH-----ENLSNEVDVRYKKNDNSMQVELRHL 108
Db 60 DSCMERILERYLYSKGLVGRDVSQSENWVLEHAKUKARVEVLEKKN-----RNF 112
Qy 109 KGEDITSANHEVLMALFEALENGLSIRDKQS---KFVDMRDNGKALEDENKRLTYEL 164
Db 113 MGEDLSLSLQSLQSLHQLDAIKSIRSKNQAMFESISALQKDKALQDHNSLL---- 169
Qy 165 QKQEMKIKENVRNMGYHQRLGNVNNNQOIPFAFRVQPIQPNLQRI 215
Db 170 -----KKIKE--REKKTQGGQGLVQCSNSSVLLPQYCVTSRDFVERV 213

RESULT 13
US-08-592-214A-10
; Sequence 10, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9001
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-592-214A-10

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-592-214A-10

Query Match          29.1%; Score 321; DB 2; Length 255;
Best Local Similarity 35.9%; Pred. No. 1.4e-22;
Matches 80; Conservative 49; Mismatches 68; Indels 26; Gaps 8;

Qy 1 MGRGKVEIKRIENSSNRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQVYCSF 60
Db 1 MGRGVQLKRIENKINRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQVYCSF 60
Qy 61 STTLTEILDKYHQS---GKGLWDKDH-----ENLSNEVDVRYKKNDNSMQVELRHL 113
Db 61 S-CMEKVLERYVSYAERQLIAPDSHVNAQTNSMEYSLKAKIELLERNQRYLGEEL 119
Qy 114 TSLNHEVLMALFEALENGLSIRDKQS---VDMRDNGKALEDENKRLTYELQKQE 169
Db 120 BPSMKDLQNLQLEQLETAHKHRSKNQLMNESLNHLQKEKEIQEENSMLT-----KQ 173
Qy 170 MKIKENVRNMGYHQRLGNVNNNQOIPFAFRVQPIQ-PNL 211
Db 174 IKERENILKTK---QTQCEQLNRSVDDVP---QPQFQPHL 209

RESULT 14
US-08-659-188-10
; Sequence 10, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-188-10

Query Match          29.1%; Score 321; DB 3; Length 255;
Best Local Similarity 35.9%; Pred. No. 1.4e-22;
Matches 80; Conservative 49; Mismatches 68; Indels 26; Gaps 8;

Qy 1 MGRGKVEIKRIENSSNRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQVYCSF 60

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Db 174 IKERENILKTK-----QTQCEQLNRSVDDVP---QPQPFQHPHL 209
Search completed: September 27, 2004, 09:30:02
Job time : 23.1253 secs

Db 1 MGRGRVELKRIENKINQVTFESKRTGLLKKAAQETSVLCDAEVSILVFSHGKGLFEYSSE 60
QY 61 STTLTEILDYKHQS---GKKLWDKXH---ENLSNEVDVKKKNDMSQVVELRLKGBDI 113
Db 61 S-CMEKVLERYERYAERQIAPDSHVAQTNWMEYSRLKAKIELLERNQRHYLGBEL 119
QY 114 TSLNHVELMALEALENGILTSIRDKQSF---VDMMDNGKALEDENKRLITYELQKQOE 169
Db 120 EPMSLKDLQNLQEQLETALKHRSRKNQNLNBSLNLHQLRKEKEIQEENSMLT-----KQ 173
QY 170 MKIKENVRNMENGYHQRLQGNYNNNQQQIPFAFRVQPIQ-PNL 211
Db 174 IKERENILKTK-----QTQCEQLNRSVDDVP---QPQPFQHPHL 209

RESULT 15
US-08-655-227-10
; Sequence 10, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-227-10

Query Match 29.1%; Score 321; DB 3; Length 255;
Best Local Similarity 35.9%; Pred. No. 1.4e-22;
Matches 80; Conservative 49; Mismatches 68; Indels 26; Gaps 8;
QY 1 MGRGKVEIKRIENSNQVTSYKRNGLIIKAKITVLCDKAKVSLIYSSSGKMEVCSP 60
Db 1 MGRGRVELKRIENKINQVTFESKRTGLLKKAAQETSVLCDAEVSILVFSHGKGLFEYSSE 60
QY 61 STTLTEILDYKHQS---GKKLWDKXH---ENLSNEVDVKKKNDMSQVVELRLKGBDI 113
Db 61 S-CMEKVLERYERYAERQIAPDSHVAQTNWMEYSRLKAKIELLERNQRHYLGBEL 119
QY 114 TSLNHVELMALEALENGILTSIRDKQSF---VDMMDNGKALEDENKRLITYELQKQOE 169
Db 120 EPMSLKDLQNLQEQLETALKHRSRKNQNLNBSLNLHQLRKEKEIQEENSMLT-----KQ 173
QY 170 MKIKENVRNMENGYHQRLQGNYNNNQQQIPFAFRVQPIQ-PNL 211

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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:10:49 ; Search time 85.6152 Seconds
(without alignments)
709.543 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103

Sequence: 1 MGRGKVEIKRIENSSNRQVT.....QQIPFAFRVQPIQPNLQERI 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	215	4	AAU00186
2	684.5	62.1	210	2	AA46555 fbp1, for
3	660.5	59.9	208	3	AA821899 Arabidops
4	650	58.9	209	5	ABG60941 Novel flo
5	650	58.9	260	5	ABG60932 Novel flo
6	645	58.5	209	5	ABG60942 Novel flo
7	640	58.0	209	5	ABG60945 Novel flo
8	639.5	58.0	212	3	AA40904 Zea mays
9	623	56.5	209	5	AAE25756 Corn AP3
10	435.5	39.5	155	3	AA821900 Arabidops
11	406.5	36.9	224	5	AAE25763 Rice MADS
12	401.5	36.4	147	3	AA821901 Arabidops
13	398.5	36.1	227	5	AAE25755 Corn AP3
14	377.5	34.2	231	2	AA43385 Product o
15	377	34.2	227	5	AAE25757 Soybean A
16	358.5	32.5	233	3	AB32552 Eucalyptu
17	358	32.5	227	4	AA68435 Amino aci
18	358	32.5	227	5	ABG30865 Poplar pr
19	358	32.5	227	7	ABU61893 Poplar ho
20	357.5	32.4	232	3	AA825577 Arabidops
21	357.5	32.4	242	3	AA825576 Arabidops
22	356.5	32.3	232	3	AA854029 Arabidops
23	356.5	32.3	236	3	AA854679 Arabidops
24	356.5	32.3	241	3	AA854028 Arabidops
25	355.5	32.2	232	4	AAU00187 Granny Sm

26	354	32.1	171	3	AA825218
27	354	32.1	181	3	AA825217
28	353.5	32.0	267	4	AA873250
29	352	31.9	227	3	AA858654
30	349.5	31.7	270	4	AA868357
31	346	31.4	273	2	AAW23814
32	346	31.4	273	2	AAW69328
33	346	31.4	273	2	AAW43112
34	346	31.4	273	2	AAW43329
35	346	31.4	273	2	AAW39134
36	346	31.4	273	3	AA867553
37	346	31.4	273	3	AA818244
38	346	31.4	273	3	AA878883
39	345.5	31.3	262	3	AA869920
40	337	30.6	238	5	AAU92966
41	337	30.6	238	7	ADC46635
42	337	30.6	238	7	ADD30296
43	335.5	30.4	250	3	AA817604
44	335.5	30.4	260	3	AA817603
45	335.5	30.4	269	3	AA84911

ALIGNMENTS

RESULT 1

AAU00186
ID AAU00186 standard; peptide; 215 AA.

XX AC AAU00186;

XX DT 11-SEP-2003 (revised)

XX DT 17-MAY-2001 (first entry)

XX XX

XX DE Granny Smith apple MdPI protein.

XX KW Granny Smith apple; MdPI; seedless fruit; horticulture;

XX KW accelerated breeding programme; cross pollination; transgenic plant;

XX KW biennial bearing tendency; codling moth.

XX OS Malus x domestica; var. Granny Smith.

XX XX

XX PN WO200117334-A1.

XX PD 15-MAR-2001.

XX PF 07-SEP-2000; 2000WO-NZ000176.

XX PR 07-SEP-1999; 99NZ-00337688.

XX PA (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.

XX PI Yao J, Morris BA;

XX DR WPI; 2001-235145/24.

XX N-PSDB; AAS00103.

XX PT New genetically modified fruiting plants that does not functionally

XX PT express MdPI or MdAP3 peptides, useful for producing seedless fruits,

XX XX specifically apple and its related species.

XX PS Claim 1; Fig 2; 4ipp; English.

XX CC The sequence represents Granny Smith apple MdPI. The invention concerns a

XX CC fruiting plant that has been genetically modified so that it does not

XX CC functionally express the MdPI or MdAP3 peptide, producing seedless

XX CC fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3

XX CC may be used to transform fruiting plants, specifically apple and pear.

XX CC The polynucleotides may be used in modulating, reducing or eliminating

XX CC seed-bearing capacity in fruiting plants, used in horticulture, and in

XX CC breeding programmes to monitor the progress in breeding a stable seedless

XX CC fruiting plant. The polynucleotides may also be used in programmes for

XX CC identifying nucleic acid variants from fruiting plants. They can be used

CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
 CC for use in an accelerated breeding programme to produce seedless fruit.
 CC They may also be used in designing probes and primers for MdPI or MdAP3,
 CC or their variants. The seedless fruiting plant is more convenient than
 CC seeded fruit since these can be cropped without pollination, reducing
 CC dependence on bees, pollinator varieties and warm weather at flowering.
 CC The absence of pollen is also advantageous to alleviate environmental
 CC concerns regarding the transfer of transgenes to non-transgenics by cross
 CC pollination. Seedless cultivars can also avoid or reduce biennial bearing
 CC tendencies that have been attributed to the inhibition of flower bud
 CC formation by developing seeds and are less susceptible to codling moth
 CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 XX Sequence 215 AA;

Query Match 100.0%; Score 1103; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.2e-87;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRGKVEIKRIENSNRQVTSKRRNGIHKAKEITVLCDAKVSIIYSSSGRWVYCSP 60
 DB 1 MGRGKVEIKRIENSNRQVTSKRRNGIHKAKEITVLCDAKVSIIYSSSGRWVYCSP 60
 QY 61 STTILTEILDKYHGSQKKLWDAKHENLSNEVDVRYKKNDNSQVLELHKGEDITSLNHYE 120
 DB 61 STTILTEILDKYHGSQKKLWDAKHENLSNEVDVRYKKNDNSQVLELHKGEDITSLNHYE 120
 QY 121 LMALEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQEMKIKENVRNME 180
 DB 121 LMALEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQEMKIKENVRNME 180
 QY 181 NGYHQRLGNYNNQOQIPFAFRVQIPQNLQERI 215
 DB 181 NGYHQRLGNYNNQOQIPFAFRVQIPQNLQERI 215

RESULT 2
 AAR46555
 ID AAR46555 standard; protein; 210 AA.
 AC AAR46555;

DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 25-JUN-1994 (first entry)

XX fbpl, for reverse genetic techniques.

XX Flower; morphology; petals; MADS box protein; toxin gene; insect;
 XX resistance; Frankliniella occidentals; plant.

XX Petunia x hybrida.

XX WO9400582-A2.

XX 06-JAN-1994.

XX 07-JUN-1993; 93WO-NL000121.

XX 30-JUN-1992; 92EP-00201951.

XX (CPRO-) CPRO-DLO CENT PLANT BREEDING & REPRODUCT.

XX Van Tunen AJ, Mollema C, Angenent GC, Dons JUM;

XX WPI; 1994-026218/03.

XX DR N-PSDB; AAQ55089.

XX New nucleic acid which alters flower morphology - by suppressing petals
 XX and stamen(s), or converts them to other organs, partic. to produce
 XX transgenic plants less susceptible to insect pests.

PS Disclosure; Fig 1A; 33pp; English.

XX A flower specific gene fbpl was isolated from the genome of Petunia
 CC hybrida. This gene has the features of a transcription factor and belongs
 CC to the group of MADS box genes. The fbpl gene is only active during
 CC differentiation of floral organ primordia and plays a crucial role in the
 CC determination of part of the floral meristem into petals and stamen
 CC primordia. Plants transformed with the gene are less attractive to insect
 CC pests so have better resistance to them; specifically cucumber plants are
 CC protected against Frankliniella occidentals but the method can be used
 CC for other, esp. parthenocarpic and/or apomictic plants. The plants are
 CC also less susceptible to secondary fungal infection. Elimination of
 CC petals may improve photosynthesis and seed yield may be increased. See
 CC also AAR46556-7. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 16-OCT-2003 to standardise OS field)
 XX
 XX Sequence 210 AA;

Query Match 62.1%; Score 584.5; DB 2; Length 210;
 Best Local Similarity 62.3%; Pred. No. 2.5e-51;
 Matches 134; Conservative 43; Mismatches 33; Indels 5; Gaps 2;
 QY 1 MGRGKVEIKRIENSNRQVTSKRRNGIHKAKEITVLCDAKVSIIYSSSGRWVYCSP 60
 DB 1 MGRGKVEIKRIENSNRQVTSKRRNGIHKAKEITVLCDAKVSIIYSSSGRWVYCSP 60
 QY 61 STTILTEILDKYHGSQKKLWDAKHENLSNEVDVRYKKNDNSQVLELHKGEDITSLNHYE 120
 DB 59 STSLVDILDQYHKLTVGRLLDPAKHENLDNEINKYKNDNNQIHLRLHKGEDITSLNHRE 118
 QY 121 LMALEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQEMKIKENVRNME 180
 DB 119 LMILEDALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQEMKIKENVRNME 178
 QY 181 NGYHQRLGNYNNQOQIPFAFRVQIPQNLQERI 215
 DB 179 EVFQORENHDYQNH--MPPAFRVQPMQPNLQERL 210

RESULT 3

AAG21899

ID AAG21899 standard; protein; 208 AA.

AC AAG21899;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 24625.

XX Protein identification; signal transduction pathway; metabolic pathway;
 XX hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139453P.
PR 16-JUN-1999; 99US-0139452P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
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PR 18-JUN-1999; 99US-0139459P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139859P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
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PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
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PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0158458P.
PR 29-SEP-1999; 99US-0158596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
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PR 14-OCT-1999; 99US-0159331P.

PR 14-OCT-1999; 99US-0159637P.
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 PR 18-OCT-1999; 99US-0159584P.
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 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
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 PR 25-OCT-1999; 99US-0161405P.
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 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161931P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 59.9%; Score 660.5; DB 3; Length 208;
 Best Local Similarity 60.5%; Pred. No. 3e-49;
 Matches 130; Conservative 33; Mismatches 39; Indels 13; Gaps 2;

QY 1 MGRGKVEIKRIENSNROVTVSKRRNGIILKKAKEITVLCDAKVSIIYSSGGMWVCSP 60
 DB 1 MGRGKVEIKRIENSNROVTVSKRRNGIILKKAKEITVLCDAKVSIIYSSGGMWVCSP 60
 QY 61 STTLTEILDYKHGSGKKLWDKAKHENSNEVDKVKDNDMSQVLRHLKGEDITSLNHYE 120
 DB 61 SMDLGAMLDQYKLSGKKLWDKAKHENSNEVDKVKDNDMSQVLRHLKGEDITSLNHYE 120
 QY 121 LMALEALENGLSIRDKOSKFVDMRDNGKALEDENKELTVELQKQEMKIKENVRNVE 180
 DB 121 LMAVEAIEHGLDKVRDHQHEIILSKRRNEKQMAEQRQLTFQLO-QQEMAIASARGMM 179
 QY 181 NGYHQRLGNYNNOQIIPFAFRVQPIQPNLQEI 215
 DB 180 MRHDGQ-----FGYRVQPIQPNLQEI 202

RESULT 4
 ABG60941
 ID ABG60941 standard; protein; 209 AA.

AC ABG60941;
 XX
 DT 27-AUG-2002 (first entry)
 XX

DE Novel floral meristem identity protein LpMADS1.

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein.
 XX
 OS Lolium perenne.
 XX
 XX WO200233091-A1.
 XX
 XX 25-APR-2002.
 PD
 XX 17-OCT-2001; 2001WO-AU001311.
 XX
 XX 19-OCT-2000; 2000AU-00000873.
 PR
 XX

PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX
 PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX
 DR WPI: 2002-454601/48.
 DR N-PSDB; ABR82124.
 XX

PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX

PS Claim 16; Fig 55; 290pp; English.

XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This is the amino acid sequence of a novel
 CC floral meristem identity protein involved in floral development and a
 CC potential target for manipulating plant life cycles
 XX

SQ Sequence 209 AA;

Query Match 58.9%; Score 650; DB 5; Length 209;
 Best Local Similarity 57.3%; Pred. No. 2.5e-48;
 Matches 122; Conservative 42; Mismatches 43; Indels 6; Gaps 2;

QY 1 MGRGKVEIKRIENSNROVTVSKRRNGIILKKAKEITVLCDAKVSIIYSSGGMWVCSP 60
 DB 1 MGRGKVEIKRIENSNROVTVSKRRNGIILKKAKEITVLCDAKVSIIYSSGGMWVCSP 60
 QY 61 STTLTEILDYKHGSGKKLWDKAKHENSNEVDKVKDNDMSQVLRHLKGEDITSLNHYE 120
 DB 61 KTSLSRILEKYQTNNGKILWDEKXKLSAEIDRIKENDNMQIELRHLKGEDINSIQPK 120
 QY 121 LMALEALENGLSIRDKOSKFVDMRDNGKALEDENKELTVELQKQEMKIKENVRNVE 180
 DB 121 LIMEEALDNGLTGLHEKQHEHYDRUMTKGMDLENDENKULAFKLH-QQDIALNGNNRELE 179
 QY 181 NGYHQRLGNYNNOQIIPFAFRVQPIQPNLQEI 213
 DB 180 LGYHPDR-----DFAAQMPITTFRVQSPSHNLQEI 207

RESULT 5
 ABG60932
 ID ABG60932 standard; protein; 260 AA.

AC ABG60932;
 XX 27-AUG-2002 (first entry)
 DT
 DE Novel floral meristem identity protein LpMADS1.
 XX
 XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein.
 XX
 OS Lolium perenne.
 XX
 XX WO200233091-A1.
 PN
 XX
 XX 25-APR-2002.
 PD
 XX
 XX 17-OCT-2001; 2001WO-AU001311.
 PF
 XX
 XX 19-OCT-2000; 2000AU-00000873.
 PR
 XX
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 PA
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PI
 XX WPI; 2002-454601/48.
 XX N-PSDB; ABK82086.
 DR
 DR New substantially purified or isolated polypeptide e.g., MADS-box,
 XX CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 PT
 XX Claim 16; Fig 28; 290pp; English.
 PS
 XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (i), a construct (iii) comprising (ii), or a
 CC vector (iv) comprising (ii), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (ii), (iii) or (iv) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced biomass in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This is the amino acid sequence of a novel
 CC floral meristem identity protein involved in floral development and a
 CC potential target for manipulating plant life cycles
 XX
 SQ Sequence 260 AA;

Query Match 58.9%; Score 650; DS 5; Length 260;
 Best Local Similarity 57.3%; Pred. No. 3.4e-48;
 Matches: 122; Conservative 42; Mismatches 43; Indels 6; Gaps 2;
 QY 1 MGRGKVEIKRIENSNQVYTKRNGIILKAKKKEITVCDKYSLLIYSSGKQVEXCSP 60
 DB 28 MGRGKIEIKRIENSNQVYTKRNGIILKAKKKEISVLCDAEYGVVVFSSAGKLYDFCSP 87
 QY 61 STLTLEILDKYHGGKGLMDAKHENLSNEVDVRVKDNDNSQVLEHLKGEDITSLNHVE 120
 DB 88 KTSLSRILEKYQVNSGKILMDKHSLSAEIDRIKKENDNMQIELHLKGEDLSLPKE 147
 QY 121 LMALEALENGLTISIRDKQSKFVDMMDNDNGKALEDENKRLTYELQKQEMKIKENVME 180
 DB 148 LIMTEALDNGLTGLHEKQMEHYDLMTKGLMDENKLLAFKLH-QDDIALNGNMELE 206
 QY 181 NGYHQRLQGNVNNQQIIPAFRVPQIPNLOE 213
 DB 207 LGYHPDR-----DFAAQNPITFRVQPSHPNLOE 234
 RESULT 6
 ABG60942
 ID ABG60942 standard; protein; 209 AA.
 XX
 AC ABG60942;
 XX
 XX 27-AUG-2002 (first entry)
 DT
 DE Novel floral meristem identity protein LpMADS1b.
 XX
 XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein.
 XX
 OS Lolium perenne.
 XX
 XX WO200233091-A1.
 PN
 XX
 XX 25-APR-2002.
 PD
 XX
 XX 17-OCT-2001; 2001WO-AU001311.
 PF
 XX
 XX 19-OCT-2000; 2000AU-00000873.
 PR
 XX
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 PA
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PI
 XX WPI; 2002-454601/48.
 XX N-PSDB; ABK82125.
 DR
 DR New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 PT
 XX Claim 16; Fig 60; 290pp; English.
 PS
 XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (i), a construct (iii) comprising (ii), or a
 CC vector (iv) comprising (ii), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (ii), (iii) or (iv) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced biomass in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This is the amino acid sequence of a novel
 CC floral meristem identity protein involved in floral development and a
 CC potential target for manipulating plant life cycles
 XX
 SQ Sequence 260 AA;

architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in the number of floral organs and flowering architecture. Manipulation of flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase biomass production; size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This is the amino acid sequence of a novel floral meristem identity protein involved in floral development and a potential target for manipulating plant life cycles

Sequence 209 AA;

Query Match 58.5%; Score 645; DB 5; Length 209;
Best Local Similarity 57.3%; Pred. No. 6.8e-48;
Matches 122; Conservative 41; Mismatches 44; Indels 6; Gaps 2;
QY 1 MGRGKVEIKRIENSNRQVTYKRRNGITKAKEITVLCDAKVSLIIYSSGKRWVEYCSF 60
DB 1 MGRGKVEIKRIENSNRQVTYKRRNGITKAKEITVLCDAKVSLIIYSSGKRWVEYCSF 60
QY 61 STLTITLTDYKHGSGKGLWDKHNLSNEVDKVDKNDNSMOVELHKLKGEDITSLNHYE 120
DB 61 KTSLSRLILEKYQNTSGKILWDEKHSLSAEIDRIKENNMQIELHKLKGEDINSLOPKX 120
QY 121 LMALEEALNGLTSIRDKSKFVDMRDNGKALEDENKELTYELOKQEMKIKENVRNME 180
DB 121 LIMIEEALDNLGLTGLHEKQMEHYDRLMTKGMLEDENKLLASKLH-QQDIALNGNRELE 179
QY 181 NGYHQRLGNYNQIQIPFAFRVQIPQNLQE 213
DB 180 LGYHPDR-----DFAAQMPITFRVQPSHPNLQE 207

RESULT 7
ABG60945

ID ABG60945 standard; protein; 209 AA.

AC ABG60945;

DT 27-AUG-2002 (first entry)

XX Novel floral meristem identity protein LpMADS2-3.

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
XX CEN-like protein; APTAL2; AP2; AP2-like protein; HB; Homeo-box protein;
XX HB-like protein; plant growth; plant architecture;
XX inflorescence development; flower development; embryo development;
XX seed development; flower organ identity; phase change; male sterility;
XX hybrid seed production; herbage quality; early maturing crop;
XX biomass increase; branching increase; blocking flowering;
XX allergenic pollen; floral meristem identity protein.

OS Lolium perenne.

XX WO200233091-A1.

XX 25-APR-2002.

XX 17-OCT-2001; 2001WO-AU001311.

PR 19-OCT-2000; 2000AU-C0000873.
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRISearch LTD.
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
PI MPI; 2002-454601/48.
XX N-PSDB; ABK82128.
DR New substantially purified or isolated polypeptide e.g. MADS-box,
XX CENTRORADIALIS, APTAL2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.
XX Claim 16; Fig 73; 290pp; English.

The invention describes a substantially purified or isolated polypeptide (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, APTAL2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a vector (IV) comprising (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in the number of floral organs and flowering architecture. Manipulation of flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase biomass production; size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This is the amino acid sequence of a novel floral meristem identity protein involved in floral development and a potential target for manipulating plant life cycles

Sequence 209 AA;

Query Match 58.0%; Score 640; DB 5; Length 209;
Best Local Similarity 56.8%; Pred. No. 1.8e-47;
Matches 121; Conservative 41; Mismatches 45; Indels 6; Gaps 2;
QY 1 MGRGKVEIKRIENSNRQVTYKRRNGITKAKEITVLCDAKVSLIIYSSGKRWVEYCSF 60
DB 1 MGRGKVEIKRIENSNRQVTYKRRNGITKAKEITVLCDAKVSLIIYSSGKRWVEYCSF 60
QY 61 STLTITLTDYKHGSGKGLWDKHNLSNEVDKVDKNDNSMOVELHKLKGEDITSLNHYE 120
DB 61 KTSLSRLILEKYQNTSGKILWDEKHSLSAEIDRIKENNMQIELHKLKGEDINSLOPKX 120
QY 121 LMALEEALNGLTSIRDKSKFVDMRDNGKALEDENKELTYELOKQEMKIKENVRNME 180
DB 121 LIMIEEALDNLGLTGLHEKQMEHYDRLMTKGMLEDENKLLASKLH-QQDIALNGNRELE 179
QY 181 NGYHQRLGNYNQIQIPFAFRVQIPQNLQE 213
DB 180 LGYHPDR-----DFAAQMPITFRVQPSHPNLQE 207

RESULT 8
AAG40904

ID	AAG40904 standard; protein; 212 AA.
XX	AAG40904;
AC	(first entry)
DT	18-OCT-2000
TX	Zea mays protein fragment SEQ ID NO: 50817.
DE	Zea mays subsp. mays.
XX	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence; corn.
XX	
OS	Zea mays subsp. mays.
PN	EP1033405-A2.
PD	06-SEP-2000.
PF	25-FEB-2000; 2000EP-00301439.
XX	
PR	25-FEB-1999; 99US-0121825P.
PR	05-MAR-1999; 99US-0123180P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	28-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127462P.
PR	08-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0129845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	23-APR-1999; 99US-0130510P.
PR	28-APR-1999; 99US-0130891P.
PR	30-APR-1999; 99US-0131449P.
PR	30-APR-1999; 99US-01322048P.
PR	04-MAY-1999; 99US-0132407P.
PR	05-MAY-1999; 99US-0132484P.
PR	06-MAY-1999; 99US-0132486P.
PR	07-MAY-1999; 99US-0132857P.
PR	11-MAY-1999; 99US-0132863P.
PR	14-MAY-1999; 99US-0134218P.
PR	14-MAY-1999; 99US-0134219P.
PR	14-MAY-1999; 99US-0134221P.
PR	18-MAY-1999; 99US-0134370P.
PR	19-MAY-1999; 99US-0134768P.
PR	20-MAY-1999; 99US-0134941P.
PR	21-MAY-1999; 99US-01351124P.
PR	24-MAY-1999; 99US-0135353P.
PR	25-MAY-1999; 99US-0135629P.
PR	27-MAY-1999; 99US-0136021P.
PR	28-MAY-1999; 99US-0136332P.
PR	03-JUN-1999; 99US-0137222P.
PR	03-JUN-1999; 99US-0137528P.
PR	04-JUN-1999; 99US-0137502P.
PR	07-JUN-1999; 99US-0137724P.
PR	08-JUN-1999; 99US-0138094P.
PR	10-JUN-1999; 99US-0138540P.
PR	14-JUN-1999; 99US-0138847P.
PR	16-JUN-1999; 99US-0139452P.
PR	16-JUN-1999; 99US-0139453P.
PR	17-JUN-1999; 99US-0139492P.
PR	18-JUN-1999; 99US-0139454P.
PR	18-JUN-1999; 99US-0139455P.
PR	18-JUN-1999; 99US-0139456P.
PR	18-JUN-1999; 99US-0139457P.
PR	18-JUN-1999; 99US-0139458P.
PR	18-JUN-1999; 99US-0139459P.
PR	18-JUN-1999; 99US-0139460P.
PR	18-JUN-1999; 99US-0139461P.
PR	18-JUN-1999; 99US-0139462P.
PR	18-JUN-1999; 99US-0139463P.
PR	18-JUN-1999; 99US-0139464P.
PR	18-JUN-1999; 99US-0139465P.
PR	18-JUN-1999; 99US-0139466P.
PR	18-JUN-1999; 99US-0139467P.
PR	18-JUN-1999; 99US-0139468P.
PR	18-JUN-1999; 99US-0139469P.
PR	18-JUN-1999; 99US-0139470P.
PR	18-JUN-1999; 99US-0139471P.
PR	18-JUN-1999; 99US-0139472P.
PR	18-JUN-1999; 99US-0139473P.
PR	18-JUN-1999; 99US-0139474P.
PR	18-JUN-1999; 99US-0139475P.
PR	18-JUN-1999; 99US-0139476P.
PR	18-JUN-1999; 99US-0139477P.
PR	18-JUN-1999; 99US-0139478P.
PR	18-JUN-1999; 99US-0139479P.
PR	18-JUN-1999; 99US-0139480P.
PR	18-JUN-1999; 99US-0139481P.
PR	18-JUN-1999; 99US-0139482P.
PR	18-JUN-1999; 99US-0139483P.
PR	18-JUN-1999; 99US-0139484P.
PR	18-JUN-1999; 99US-0139485P.
PR	18-JUN-1999; 99US-0139486P.
PR	18-JUN-1999; 99US-0139487P.
PR	18-JUN-1999; 99US-0139488P.
PR	18-JUN-1999; 99US-0139489P.
PR	18-JUN-1999; 99US-0139490P.
PR	18-JUN-1999; 99US-0139491P.
PR	18-JUN-1999; 99US-0139492P.
PR	18-JUN-1999; 99US-0139493P.
PR	18-JUN-1999; 99US-0139494P.
PR	18-JUN-1999; 99US-0139495P.
PR	18-JUN-1999; 99US-0139496P.
PR	18-JUN-1999; 99US-0139497P.
PR	18-JUN-1999; 99US-0139498P.
PR	18-JUN-1999; 99US-0139499P.
PR	18-JUN-1999; 99US-0139500P.
PR	18-JUN-1999; 99US-0139501P.
PR	18-JUN-1999; 99US-0139502P.
PR	18-JUN-1999; 99US-0139503P.
PR	18-JUN-1999; 99US-0139504P.
PR	18-JUN-1999; 99US-0139505P.
PR	18-JUN-1999; 99US-0139506P.
PR	18-JUN-1999; 99US-0139507P.
PR	18-JUN-1999; 99US-0139508P.
PR	18-JUN-1999; 99US-0139509P.

PR	23-AUG-1999;	99US-0149930P.	DB	180	TCYHQVQ--HSDRFISQMPFTFRVQPNHPNLQE	210
PR	25-AUG-1999;	99US-0150566P.				
PR	26-AUG-1999;	99US-0150884P.				
PR	27-AUG-1999;	99US-0151065P.				
PR	27-AUG-1999;	99US-0151066P.				
PR	27-AUG-1999;	99US-0151080P.				
PR	30-AUG-1999;	99US-0151303P.				
PR	31-AUG-1999;	99US-0151438P.				
PR	01-SEP-1999;	99US-0151930P.				
PR	07-SEP-1999;	99US-0152363P.				
PR	10-SEP-1999;	99US-0153070P.				
PR	13-SEP-1999;	99US-0153758P.				
PR	15-SEP-1999;	99US-0154018P.				
PR	16-SEP-1999;	99US-0154039P.				
PR	20-SEP-1999;	99US-0154779P.				
PR	22-SEP-1999;	99US-0155139P.				
PR	23-SEP-1999;	99US-0155486P.				
PR	24-SEP-1999;	99US-0155659P.				
PR	28-SEP-1999;	99US-0156458P.				
PR	29-SEP-1999;	99US-0156596P.				
PR	04-OCT-1999;	99US-0157117P.				
PR	05-OCT-1999;	99US-0157753P.				
PR	06-OCT-1999;	99US-0157865P.				
PR	07-OCT-1999;	99US-0158029P.				
PR	08-OCT-1999;	99US-0158232P.				
PR	12-OCT-1999;	99US-0158369P.				
PR	13-OCT-1999;	99US-0159293P.				
PR	13-OCT-1999;	99US-0159294P.				
PR	13-OCT-1999;	99US-0159295P.				
PR	14-OCT-1999;	99US-0159329P.				
PR	14-OCT-1999;	99US-0159330P.				
PR	14-OCT-1999;	99US-0159331P.				
PR	14-OCT-1999;	99US-0159637P.				
PR	14-OCT-1999;	99US-0159638P.				
PR	18-OCT-1999;	99US-0159884P.				
PR	21-OCT-1999;	99US-0160741P.				
PR	21-OCT-1999;	99US-0160767P.				
PR	21-OCT-1999;	99US-0160768P.				
PR	21-OCT-1999;	99US-0160770P.				
PR	21-OCT-1999;	99US-0160814P.				
PR	21-OCT-1999;	99US-0160815P.				
PR	22-OCT-1999;	99US-0160980P.				
PR	22-OCT-1999;	99US-0160981P.				
PR	22-OCT-1999;	99US-0160989P.				
PR	23-OCT-1999;	99US-0161404P.				
PR	25-OCT-1999;	99US-0161405P.				
PR	25-OCT-1999;	99US-0161406P.				
PR	26-OCT-1999;	99US-0161359P.				
PR	26-OCT-1999;	99US-0161360P.				
PR	26-OCT-1999;	99US-0161361P.				
PR	28-OCT-1999;	99US-0161920P.				
PR	28-OCT-1999;	99US-0161992P.				
PR	28-OCT-1999;	99US-0161993P.				
PR	29-OCT-1999;	99US-0162142P.				
<p>Query Match 58.0%; Score 639.5; DB 3; Length 212; Best Local Similarity 58.8%; Pred. No. 2.1e-47; Matches 124; Conservative 39; Mismatches 47; Indels 3; Gaps 2;</p>						
QY	1	MGRGKVEIKRIENSSNRQVTYSKRRNGIIRKKAKEITVLCDAKVSLIIYSSSGKMWVCSP	60			
DB	1	MGRGKVEIKRIENSTNRQVTFKRRAGLVKKAKEICVLCDAEVGVVIFSSGKLYDYCSP	60			
QY	61	STILTILDKYHCQSGKLDKAKHNLNEVDKVKNDMSQVLRHLKGEDITSLNHYE	120			
DB	61	RYSLSILEKYQNSGKILWGEKHLSAEIDRVKENDNMQIQLRHLKGEDLSLQPRE	120			
QY	121	LMALAEALENGLTISIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME	180			
DB	121	LTAIEGLQNGQTNREKQDYWRHTTNGKVKLEDEHKILIFRMH-QQAVDLSGGMRELE	179			
QY	181	NGYHQQLGNVNNQOQIIPFAPRVPQIQNLQE	213			
<p>Query Match 56.5%; Score 623; DB 5; Length 209; Best Local Similarity 55.8%; Pred. No. 5.5e-46; Matches 119; Conservative 45; Mismatches 42; Indels 8; Gaps 3;</p>						
QY	1	MGRGKVEIKRIENSSNRQVTYSKRRNGIIRKKAKEITVLCDAKVSLIIYSSSGKMWVCSP	60			
DB	1	MGRGKVEIKRIENSTNRQVTFKRRNGILKKAKEISVLCDAEVGVVIFSSACKLYDYCSP	60			
QY	61	STILTILDKYHCQSGKLDKAKHNLNEVDKVKNDMSQVLRHLKGEDITSLNHYE	120			
DB	61	KTSLSKILEKYQNSGKILWGEKHLSAEIDRIKENDTMQIELRHLKGEDLSLQPKD	120			
QY	121	LMALAEALENGLTISIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME	180			

Db 180 TCYHQVQ--HSDRFISQMPFTFRVQPNHPNLQE 210

RESULT 9

AAE25756

ID AAE25756 standard; protein; 209 AA.

AC AAE25756;

XX

DT 04-NOV-2002 (first entry)

XX

DE Corn AP3 homologue protein from clone ctnlc.pk002.j23.

XX

KW Floral developmental protein; flowering locus T; APETALA3; transgenic; FT; AP3; transgenic plant; fertility; flower development; gene mapping; sterility; plant growth; inflorescence architecture; plant morphology; tissue culture; cell division; corn.

OS Zea mays.

XX

PN WO200244390-A2.

XX

PD 06-JUN-2002.

XX

PF 21-NOV-2001; 2001WO-US043750.

XX

PR 28-NOV-2000; 2000US-0253415P.

XX

PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX

PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

XX

DR WPI, 2002-547703/58.

DR

DR N-PSDB; AAD42258.

XX

PT New floral developmental polypeptide having flowering locus T or AP3 homolog activity, useful for immunological screening of cDNA expression libraries.

XX

PS Claim 18; Page 79-80; 88pp; English.

XX

CC The present invention relates to novel floral developmental proteins, more specifically flowering locus T (FT) or APETALA3 (AP3) homologue proteins and polynucleotides encoding such proteins. Floral developmental polynucleotides are useful for transforming cells or for producing plants by transforming the plant cells with the polynucleotides and regenerating the plants from the transformed plant cells. Sequences of the invention are useful for immunological screening of cDNA expression libraries. They are also useful for creating transgenic plants. Polynucleotides of the invention are used as probes for genetically and physically mapping the genes that they are a part of and as markers for traits linked to those genes. AP3 homologues may be useful for engineering plant sterility or fertility, flower development and morphology. FT or TFL1 homologues are useful for engineering flowering time, plant growth rate, inflorescence architecture, tissue culture morphology and rate of cell division to enhance transformation. The present sequence is corn AP3 homologue protein

XX Sequence 209 AA;

Query Match 56.5%; Score 623; DB 5; Length 209;
 Best Local Similarity 55.8%; Pred. No. 5.5e-46;
 Matches 119; Conservative 45; Mismatches 42; Indels 8; Gaps 3;

QY 1 MGRGKVEIKRIENSSNRQVTYSKRRNGIIRKKAKEITVLCDAKVSLIIYSSSGKMWVCSP 60

DB 1 MGRGKVEIKRIENSTNRQVTFKRRNGILKKAKEISVLCDAEVGVVIFSSACKLYDYCSP 60

QY 61 STILTILDKYHCQSGKLDKAKHNLNEVDKVKNDMSQVLRHLKGEDITSLNHYE 120

DB 61 KTSLSKILEKYQNSGKILWGEKHLSAEIDRIKENDTMQIELRHLKGEDLSLQPKD 120

QY 121 LMALAEALENGLTISIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180

Db 121 LIMTEALDGLNLNKLMEHWRVNTKMMEDENKLIAPKLIH-QODIALSGSMRELE 179
Qy 181 NGYH-QROLGNVNNQOQIFFAFVQPIQBNLOE 213
Db 180 LGYHPRDLA-----AQMPTTRVQPSHPNLOE 207

RESULT 10

AAG21900
ID AAG21900 standard; protein; 155 AA.

XX AC AAG21900;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 24626.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.

XX OS Arabidopsis: thaliana.

XX PN EPI033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

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PR 04-MAY-1999; 99US-0132484P.

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PR 06-MAY-1999; 99US-0132486P.

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PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

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PR 25-MAY-1999; 99US-0136021P.

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PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

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PR 14-JUN-1999; 99US-0139115P.

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PR 18-JUN-1999; 99US-0139455P.

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PR 18-JUN-1999; 99US-0139458P.

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PR 18-JUN-1999; 99US-0139460P.

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PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139753P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140695P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 02-JUL-1999; 99US-0142055P.

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PR 02-AUG-1999; 99US-0146386P.

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PR 06-AUG-1999; 99US-0147303P.

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PR 09-AUG-1999; 99US-0147493P.

PR 09-AUG-1999; 99US-0147835P.

PR 10-AUG-1999; 99US-0148171P.

PR 11-AUG-1999; 99US-0148319P.

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PR 04-OCT-1999; 99US-0157117P.
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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
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PR 21-OCT-1999; 99US-0160768P.
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PR 21-OCT-1999; 99US-0160815P.
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PR 26-OCT-1999; 99US-0161360P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
PR 29-OCT-1999; 99US-0162143P.

Query Match 39.5%; Score 435.5; DB 3; Length 155;
Best Local Similarity 54.3%; Pred. No. 7.2e-30;
Matches 8; Conservative 23; Mismatches 38; Indels 13; Gaps 2;

QY 54 MVEYCSPTTLTILDKYHQSCKLWDAKHENLSNEVDVRKDNDSMQVELRHLKGEDI 113
Db 1 MIDYCCPSMDLGMLDQYQKLSGKCLWDAKHENLSNEIDRIKENDSLQELRHLKGEDI 60
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QY 114 TSLNHVELMALBEALENGLTISIRKQSKFVDMRDNGKALDENKRLTYELQKQOEMKIK 173
Db 61 QSLNLKLVNAVEHAIEHGLDKVDRHQMEILLISKRRNEQMAEEQRLTFQLQ-QQEAIA 119

QY 174 ENVRNMENGYHORGLNYYNNNQOQIPFAFRVQPIQPNLQERI 215
Db 120 SNARGMMWRDHDGQ-----FGYRVQPIQPNLQEKI 149

RESULT 11
AAE25763
ID AAE25763 standard; protein; 224 AA.
XX
AC AAE25763;
DT 04-NOV-2002 (first entry)
XX
DE Rice MADS box-like protein.
XX
KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
KW sterility; plant growth; inflorescence architecture; plant morphology;
KW tissue culture; cell division; rice; MADS box-like protein.
XX
OS Oryza sativa.
XX
PN WO200244390-A2.
XX
PD 06-JUN-2002.
XX
PF 21-NOV-2001; 2001WO-US043750.
XX
PR 28-NOV-2000; 2000US-0253445P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
XX
DR WPI; 2002-547703/58.
XX
PT New floral developmental polypeptide having flowering locus T or Ap3
PT homolog activity, useful for immunological screening of cDNA expression
PT libraries.
XX
PS Example 4; Page 82-83; 88pp; English.
XX
CC The present invention relates to novel floral developmental proteins,
CC more specifically flowering locus T (FT) or APETALA3 (AP3) homolog
CC proteins and polynucleotides encoding such proteins. Floral developmental
CC polynucleotides are useful for transforming cells or for producing plants
CC by transforming the plant cells with the polynucleotides and regenerating
CC the plants from the transformed plant cells. Sequences of the invention
CC are useful for immunological screening of cDNA expression libraries. They
CC are also useful for creating transgenic plants. Polynucleotides of the
CC invention are used as probes for genetically and physically mapping the
CC genes that they are a part of and as markers for traits linked to those
CC genes. AP3 homologues may be useful for engineering plant sterility or
CC fertility, flower development and morphology. FT or TFL1 homologues are
CC useful for engineering flowering time, plant growth rate, inflorescence
CC architecture, tissue culture morphology and rate of cell division to
CC enhance transformation. The present sequence is rice MADS box-like
CC protein. This sequence is used in the exemplification of the invention
XX
SQ Sequence 224 AA;
```

```
Query Match 36.9%; Score 406.5; DB 5; Length 224;
Best Local Similarity 40.8%; Pred. No. 3.9e-27;
Matches 89; Conservative 41; Mismatches 73; Indels 15; Gaps 4;

QY 1 MGRGKVIKRIENSNRQVTYSKRRNGIHKKEITVLCDAKYSLITYSSGKQVFCSP 60
Db 1 MGRGKIEIKRIENATNFQVTYSKRRNGIHKKEITVLCDAQVAIMFSGTKYHFCSP 60
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Qy 61 STITLITELDKYHSGSKLWDAKHENLSNEVDKVKDNDMSQVLEHLKKGEDTISLNHVE 120
Db 61 STDIKGIFDRYQQAIGTSLMIEQYENMQRTLSHLKDINRLRTEIQRMGEDLDGLEFDE 120
Qy 121 LMALEEALNGLTSIRDQSKFVDMMDRDNGKALEDENKRLTYELQK--QOEMKIKEN--- 175
Db 121 LRGLEQNVDAALKEVRHKYHVTQTETK---KKVHSYEAYETLQOELGLREPAF 176
Qy 176 --VRNMENGHQRLGNYYNNQQOIPAPRVQPIQPNL 211
Db 177 GFVDNTGGWD---GGAGAGAAADMFAPRVFSPQNL 210

RESULT 12
AAG21901
ID AAG21901 standard; protein; 147 AA.
XX AC AAG21901;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 24627.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX EN EPI033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 29-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127452P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
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PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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PR 18-MAY-1999; 99US-0134768P.
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PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 18-JUN-1999; 99US-0139454P.
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PR 18-JUN-1999; 99US-0139458P.
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PR 18-JUN-1999; 99US-0139463P.
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PR 29-JUN-1999; 99US-0140991P.
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PR 01-JUL-1999; 99US-0142154P.
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PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 19-JUL-1999; 99US-0144333P.
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PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
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PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
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PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.

Matches	88; Conservative	41; Mismatches	78; Indels	11; Gaps	3;
QY	1	MGRGKVEIKRIENSNROVTVSKRRNGIIKAKAEITVLCDAKVSIIYSSGKVEYCSP	60		
Db	1	MGRGKIEIKRIENATNRQVTVSKRTGTGMKKARELTVLDAQVAIIIMFSSTGKHEFCSP	60		
QY	61	STLTLEILDKVGHSKKLWDAKHENLSNEVDRAVKDNDMSQVELRHLKGEDITSLNHVE	120		
Db	61	GTDIKTIIFDRYQQAIGTSLWTEQYENQRTLSHLKQINRGLRTEIRQRMGEOLDSLDFDE	120		
QY	121	LMALFEALENGLTSDIRDKOSKQFVDMWDNGKALEDENKRLTVSELQK--QEMKIKEN--	175		
Db	121	LGLELQNVDAALKVEVRHKYHVIQTQTDYK---KKVKHSBAYKVLQQLGEMREDPAF	176		
QY	176	--VRNVNGYHQRLQGNWNNNQOQIIPFAFRVQFIQPNL	211		
Db	177	GVYDNTGAGVWDGAAAAALGGAPDMYAFKVPFSOPNL	214		

RESULT 14	
AA43385	
ID	AA43385 standard; protein; 231 AA.
XX	
AC	AA43385;
XX	
DT	25-MAR-2003 (revised)
DT	19-JUN-1994 (first entry)
XX	
DE	Product of homeotic gene green petal.
XX	
XX	
KW	Plant; organ morphogenesis; control; petunia; petals.
XX	
OS	Petunia.
XX	
PN	W09321322-A1.
XX	
PD	28-OCT-1993.
XX	
PF	13-APR-1993; 93WO-US003508.
XX	
PR	13-APR-1992; 92US-00867580.
PR	06-JUL-1992; 92US-00909589.
XX	
PA	(UYRQ) UNIV ROCKEFELLER.
XX	
PI	Halfter U, Van Der Krol AR, Kush A, Chua N;
XX	
DR	WPI; 1993-351732/44.
DR	N-PSDB: AAO51189.

XX plant organ morphogenesis control and determin. - by regulating the
PT expression of homeotic genes which determine the identity of the organ.
XX Disclosure: Fig 2: 74pp: English.
PS

xx The homeotic gene green petal from petunia has been cloned and
CC characterised previously. The gene was used in a new method for
CC controlling the morphogenesis of plant organs comprising regulating the
CC expression of the gene using ectopic expression. Such a method can be
CC used to determine and control plant organ morphogenesis, such as
CC modifying petals without altering the reproductive portions of the
CC flower. See also AAR43386-7. (Updated on 25-MAR-2003 to correct PN
CC field.)

AA
SQ Sequence 231 AA;
Query Match 34.2%; Score 377.5; DB 2; Length 231;
Best Local Similarity 38.5%; Pred. No. 1.3e-24;
Matches 84; Conservative 47; Mismatches 72; Indels 15; Gaps 4;

Qy

1 MGRGVEIKRIENSSNRQVTSKRRNGIIKKAEITVLCDAKYSLIIVSSSGKWVEYCSP 60
| | | | : | | | | | | | | | | | | | | | | | | | | | |
| | | | : | | | | | | | | | | | | | | | | | | | | | |

Dd

1 MARGIQIKRIENOTNRQVTSKRRNGLFFKANELTVLCDAKYSIIIMISSTGKUHEFISP 60
| | | | : | | | | | | | | | | | | | | | | | | | | | |

Query Match 34.2%; Score 377; DB 5; Length 227;
Best Local Similarity 36.4%; Pred. No. 1.4e-24;

Qy	61	STTLTEILDKYHGQGGKKLWDAKENHLSNEVDVRVKNDQSQVELRHUKGKEDTISLHNHVE	120
Db	61	STTLTEILDKYHGQGGKKLWDAKENHLSNEVDVRVKNDQSQVELRHUKGKEDTISLHNHVE	120
Db	61	SIITQFLQFLYQKTVGVDLWNSHVEKMQEQRUKKLUKLEVRNRNURKEIORMGESLUNDNYEQ	120
Qy	121	LMALAEALENGLTISIRDKQSFVDMWRDNGKALEDENKRLTYELQKQENKXIKENTVRNME	180
Db	121	LEELMENVNSLKLREKKYKVI-----GNQIETFKKKVRNBEIHRNLLLEFFDARQED	174
Qy	181	NGYHQQLGNYN-----NNQQIPFPAPRVQP--IQPN	210
Db	175	PYGLVBOEGDYNVLGFPGNGHRI-LALRLQPNHHPN	211

RESULT 15

AAE25757
ID AAE25757 standard; protein: 227 AA.

AAE25757:

XX DT 04-NOV-2002 (first entry)

DE Soybean AP3 homologue protein from clone sfl1n.pk001.116.

Floral developmental protein; flowering locus T; APETALA3; transgenic;
KW
KW FT; AP3; transgenic plant; fertility; flower development; gene mapping
KW sterility; plant growth; inflorescence architecture; plant morphology;
KW tissue culture; cell division; soybean.

Glycine max.

XX
PN
WO20024390-A2.XX
PD
06-JUN-2002XX
PF
21-NOV-2001:XX
PP 28-NOV-2000. 2000US-0253415PXX
F2 /BUDG / BY DONT DE MEMOIRS C

X

XX
XX

DR N-PSDB; AAD42259.

PT New floral developmental polypeptide having flowering locus T or Ap3
PT homolog activity, useful for immunological screening of cDNA expression
PT libraries.

XX
PS
Claim 17: Page 80-81: 88pp: English:

The present invention relates to novel floral developmental proteins, more specifically flowering locus T (FT) or AP3/APTA3 (AP3) homologue proteins and polynucleotides encoding such proteins. Floral developmental proteins and polynucleotides are useful for transforming cells or for producing plants by transforming the plant cells with the polynucleotides and regenerating the plants from the transformed plant cells. Sequences of the invention are useful for immunological screening of cDNA expression libraries. They are also useful for creating transgenic plants. Polynucleotides of the invention are used as probes for genetically and physically mapping the genes that they are a part of and as markers for traits linked to those genes. AP3 homologues may be useful for engineering plant sterility or fertility, flower development and morphology. FT or TFL1 homologues are useful for engineering flowering time, plant growth rate, inflorescence architecture, tissue culture morphology and rate of cell division to enhance transformation. The present sequence is soybean AP3 homologue protein

XX
SO
Sequence 227 AA:

Query Match

Query Match 34.2%; Score 377; DB 5; Length 227;
Best Local Similarity 36.4%; Pred. No. 1.4e-24;

Matches	78; Conservative	52; Mismatches	76; Indels	8; Gaps	3;
Qy	1 MGRGVKIKRIENSSNQVTSYKERNGIIKAKKEITVLCDAKVSLLIYSSSGHMVEYCSP	60			
Db	1 MARGKIQIKRIENNTNRQVTSYKERNGLFKKANELTVLCDAKVSIIIFSSTGKLHQYISP	60			
Qy	61 STTLTEILDYHGSGKKLMDAKHENLSNEVDVYKKNDSQVVELRHLKGEDITSLNHYE	120			
Db	61 STSTKQFFDQYQWTLGVDLWNSHYENQENLKKLKEVYRNLRKEIRQRMGDCINELGMED	120			
Qy	121 LMALEEALENGLTISIRDKQSKF----	VDMMRDNGKALEDENKRLTYELOKQOQEMKIKENV	176		
Db	121 LKLEEEEMDKAAKVVRERKYVITNQIDTQKKFNEKEVHNRLHLDLDAKAE--DPRF	177			
Qy	177 RNMENGYHQROLGNYNQOQIPAFRVQPIQPN	210			
Db	178 ALIDNGGEYSVIGFSNLGPRM-FALSIQFSHPS	210			

Search completed: September 27, 2004, 09:25:11
 Job time : 90.6152 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 20:24:57 ; Search time 455.966 Seconds
(without alignments)
9149.204 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgccgggaagattga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : N_Geneseq_25Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	982	100.0	982	4	AAS00104
2	28	2.9	1447	7	ACA96031
3	27	2.7	121	6	ABK25242
4	27	2.7	121	6	ABK25241
5	27	2.7	121	6	ABK25237
6	27	2.7	121	6	ABK25238
7	27	2.7	390	8	ACH38095
8	27	2.7	448	6	ABL93709
9	27	2.7	458	6	ABL93709
10	27	2.7	712	6	ABQ65619
11	27	2.7	980	4	AD06338
12	27	2.7	1167	2	AAT66687
13	27	2.7	1167	2	AAV69276
14	27	2.7	1167	2	AAV81423
15	27	2.7	1167	8	ADA01011
16	27	2.7	1547	6	ABN84158
17	27	2.7	17424	6	ABL68122
18	26	2.6	121	6	ABK25462
19	26	2.6	121	6	ABK25466
20	26	2.6	121	6	ABK25465
21	26	2.6	121	6	ABK25461
22	26	2.6	164	9	ADE58862
23	26	2.6	181	7	ACC60003

24	26	2.6	267	7	ACA05130	ACA05130 Rice leaf
25	26	2.6	461	6	ABL93649	ABL93649 Arabidops
26	26	2.6	487	8	ACH34795	ACH34795 Human end
27	26	2.6	552	6	ABQ57750	ABQ57750 Human col
28	26	2.6	868	4	AAS00103	AAS00103 Granny Sm
29	26	2.6	1142	6	ABN98309	ABN98309 Arabidops
30	26	2.6	1154	2	AAT39048	AAT39048 cDNA enco
31	26	2.6	1306	6	AAD42765	AAD42765 Wheat GGP
32	26	2.6	1306	6	ACA05162	ACA05162 Wheat ger
33	26	2.6	1770	5	AAF24163	AAF24163 Human sec
34	26	2.6	1819	5	AAF30436	AAF30436 Rice apop
35	26	2.6	1978	2	AAQ37189	AAQ37189 Petunia E
36	26	2.6	2645	3	AAF16125	AAF16125 Human pro
37	26	2.6	2663	4	AAD08310	AAD08310 Human sec
38	26	2.6	2844	7	ABT31903	ABT31903 Human bpc
39	26	2.6	80578	4	AAH44800	AAH44800 Human GPC
40	25	2.5	44	6	AAS17877	AAS17877 FC-3 comm
41	25	2.5	45	8	ABZ76605	ABZ76605 Human CNI
42	25	2.5	51	4	AAI29700	AAI29700 Human SNP
43	25	2.5	207	6	ABU86102	ABU86102 Human ova
44	25	2.5	269	7	ABX61308	ABX61308 Arabidops
45	25	2.5	394	5	ABV49244	ABV49244 Human pro
46	25	2.5	396	4	AAF94886	AAF94886 Human ova
47	25	2.5	396	6	ABU48836	ABU48836 Ovarian c
48	25	2.5	396	6	ABT03153	ABT03153 Human ova
49	25	2.5	423	3	AAE68807	AAE68807 Human hea
50	25	2.5	458	8	ACH21953	ACH21953 Human adu
51	25	2.5	502	5	ABV56360	ABV56360 Human pro
52	25	2.5	524	2	AAQ12088	AAQ12088 C-termina
53	25	2.5	650	3	AAQ59569	AAQ59569 Human sec
54	25	2.5	878	4	AAK64702	AAK64702 Human imm
55	25	2.5	1145	6	ABK35955	ABK35955 cDNA sequ
56	25	2.5	1146	2	AAQ07000	AAQ07000 Xenopus F
57	25	2.5	1190	2	AAZ20289	AAZ20289 Aspen hom
58	25	2.5	1347	4	AAQ86035	AAQ86035 CABP-1 co
59	25	2.5	1392	6	AAQ39218	AAQ39218 Rice tyro
60	25	2.5	1402	2	AAQ78204	AAQ78204 Soybean N
61	25	2.5	1402	4	AAE57653	AAE57653 Soybean i
62	25	2.5	1487	3	AAZ41288	AAZ41288 Human nor
63	25	2.5	1760	3	AAZ43782	AAZ43782 Human fec
64	25	2.5	1796	8	ABZ76577	ABZ76577 Human CNI
65	25	2.5	1940	2	AAQ38690	AAQ38690 Mouse CRT
66	25	2.5	1974	7	ADA56170	ADA56170 Gene enco
67	25	2.5	1974	7	ADA39981	ADA39981 Human sec
68	25	2.5	1974	7	ACC50542	ACC50542 Human sec
69	25	2.5	1974	9	ADC73606	ADC73606 Human sec
70	25	2.5	1981	3	AAA23458	AAA23458 cDNA enco
71	25	2.5	2133	9	ADD44822	ADD44822 Rat gene
72	25	2.5	2133	9	ADD44822	ADD44822 Rat gene
73	25	2.5	2149	2	AAQ87942	AAQ87942 Human cys
74	25	2.5	2212	7	ACC00727	ACC00727 Zea mays
75	25	2.5	2290	6	ABK35014	ABK35014 Human CDN
76	25	2.5	2359	9	ADB52957	ADB52957 Primary r
77	25	2.5	2396	2	AAV66452	AAV66452 An antidi
78	25	2.5	2396	2	AAQ35295	AAQ35295 Nucleic a
79	25	2.5	2396	2	AAQ35283	AAQ35283 Nucleic a
80	25	2.5	2396	3	AAA07264	AAA07264 Rice prob
81	25	2.5	2396	6	ABE57331	ABE57331 cDNA enco
82	25	2.5	4131	2	AAQ89290	AAQ89290 Dogfish s
83	25	2.5	4134	6	AAA41631	AAA41631 SKCAR DNA
84	25	2.5	4134	6	ABK14910	ABK14910 DNA enco
85	25	2.5	4134	6	ABK15964	ABK15964 Dogfish s
86	25	2.5	4134	6	ABK15964	ABK15964 Human imm
87	25	2.5	34658	4	AAK69489	AAK69489 Sense oli
88	24	2.4	40	2	AAQ22625	AAQ22625 Sense oli
89	24	2.4	47	3	AAA61350	AAA61350 Model lin
90	24	2.4	47	4	AAQ60446	AAQ60446 DNA oligo
91	24	2.4	97	2	AAQ68582	AAQ68582 Nucleotid
92	24	2.4	101	2	AAT07155	AAT07155 pV3TA-LTR
93	24	2.4	121	6	ABK25234	ABK25234 Male-ster
94	24	2.4	121	6	ABK25234	ABK25234 Male-ster
95	24	2.4	121	6	ABK25265	ABK25265 Male-ster
96	24	2.4	121	6	ABK25269	ABK25269 Male-ster
97	24	2.4	121	6	ABK25270	ABK25270 Male-ster

97	24	2.4	121	6	ABK25273	Abk25273 Male-ster	170	24	2.4	1093	7	ABZ67043	Abz67043 Human sec
98	24	2.4	121	6	ABK25266	Abk25266 Male-ster	171	24	2.4	1093	7	ADA43901	Ada43901 Human sec
99	24	2.4	121	6	ABK25274	Abk25274 Male-ster	172	24	2.4	1133	3	Aaz90586	Aaz90586 Maize pro
100	24	2.4	121	6	ABK25233	Abk25233 Male-ster	173	24	2.4	1201	2	AAx61465	AAx61465 DNA encod
101	24	2.4	121	6	ABK25262	Abk25262 Male-ster	174	24	2.4	1344	4	Aah72881	Aah72881 Human cer
102	24	2.4	121	6	ABK25261	Abk25261 Male-ster	175	24	2.4	1343	4	AAQ44450	AAQ44450 Cysteine
103	24	2.4	166	2	AAQ67613	AAQ67613 tRNA modi	176	24	2.4	1305	7	ADA09070	ADA09070 DNA encod
104	24	2.4	166	2	AAQ67614	AAQ67614 tRNA modi	177	24	2.4	1323	3	AAa61764	AAa61764 cDNA enco
105	24	2.4	169	4	AA524514	AA524514 Human ova	178	24	2.4	1430	3	AAx90911	AAx90911 Human cDN
106	24	2.4	170	5	AAH83122	AAH83122 Human ova	179	24	2.4	1439	2	AAQ92086	AAQ92086 Human cDN
107	24	2.4	185	5	ABV34436	ABV34436 Human pro	180	24	2.4	1439	2	AAQ92086	AAQ92086 Human cDN
108	24	2.4	185	5	ABV343294	ABV343294 Human pro	181	24	2.4	1486	6	AAc98137	AAc98137 Human col
109	24	2.4	192	7	ABZ78104	ABZ78104 Human sup	182	24	2.4	1507	6	ABs54111	ABs54111 Tobacco c
110	24	2.4	201	6	ABL85925	ABL85925 Human ova	183	24	2.4	1564	7	ABX78356	ABX78356 Soybean s
111	24	2.4	235	7	ABX60803	ABX60803 Arabidops	184	24	2.4	1565	8	ADD17505	ADD17505 Wheat pos
112	24	2.4	250	7	ABX98053	ABX98053 Rice endo	185	24	2.4	1588	9	ADD14723	ADD14723 Human src
113	24	2.4	293	2	AAAT07148	AAAT07148 Ribozyme-	186	24	2.4	1607	2	AAx60316	AAx60316 DNA encod
114	24	2.4	293	2	AAAT07152	AAAT07152 Ribozyme-	187	24	2.4	1624	2	AAAT39750	AAAT39750 Human muc
115	24	2.4	293	2	AAAT07151	AAAT07151 Ribozyme-	188	24	2.4	1624	2	AAx35279	AAx35279 cDNA enco
116	24	2.4	293	2	AAAT07147	AAAT07147 Ribozyme-	189	24	2.4	1646	6	ABQ88122	ABQ88122 Human ost
117	24	2.4	300	2	AAQ67610	AAQ67610 PV3TA-tat	190	24	2.4	1702	4	AAc85066	AAc85066 Atheroscl
118	24	2.4	300	2	AAQ67609	AAQ67609 PV3TA-LTR	191	24	2.4	1734	4	AAAT39792	AAAT39792 Human SH3
119	24	2.4	326	4	AAAL28279	AAAL28279 Human bre	192	24	2.4	1749	4	AAI60696	AAI60696 Human pol
120	24	2.4	328	4	AAAL08534	AAAL08534 Human bre	193	24	2.4	1755	2	AAAT91321	AAAT91321 Arabidops
121	24	2.4	345	2	AAQ67612	AAQ67612 PV3TA-tat	194	24	2.4	1760	3	AAc59930	AAc59930 Human sec
122	24	2.4	346	2	AAQ94618	AAQ94618 PV3TA-tat	195	24	2.4	1795	3	AAAT18075	AAAT18075 Lung canc
123	24	2.4	348	2	AAQ67611	AAQ67611 PV3TA-tat	196	24	2.4	1900	9	ADe61362	ADe61362 Human gen
124	24	2.4	354	7	ABZ73127	ABZ73127 Rice leaf	197	24	2.4	1971	2	AAx08428	AAx08428 Acidic le
125	24	2.4	368	4	AAAL19229	AAAL19229 Human bre	198	24	2.4	2069	1	AAAT92452	AAAT92452 cDNA inse
126	24	2.4	374	4	AAAS25015	AAAS25015 Human ova	199	24	2.4	2125	6	ABT05130	ABT05130 Cytokine
127	24	2.4	374	5	AAH83660	AAH83660 Human ova	200	24	2.4	2179	6	AAc59087	AAc59087 Human sec
128	24	2.4	381	7	ABZ73087	ABZ73087 Rice leaf	201	24	2.4	2185	3	AAc59087	AAc59087 Human sec
129	24	2.4	390	8	ACH29210	ACH29210 Human adu	202	24	2.4	2187	3	AAZ922220	AAZ922220 Human thi
130	24	2.4	391	2	AAQ94619	AAQ94619 PV3TA-tat	203	24	2.4	2187	6	AAI72951	AAI72951 Human thi
131	24	2.4	391	4	AAH33291	AAH33291 Human col	204	24	2.4	2203	2	AAZ06247	AAZ06247 Human sec
132	24	2.4	395	7	ABX62795	ABX62795 Arabidops	205	24	2.4	2217	9	ABT42483	ABT42483 Toxicity
133	24	2.4	404	8	ACH18231	ACH18231 Human adu	206	24	2.4	2217	9	ABT59228	ABT59228 Toxicity
134	24	2.4	439	5	ABV48426	ABV48426 Human pro	207	24	2.4	2298	7	ABQ84310	ABQ84310 Human DPP
135	24	2.4	448	2	AAQ94620	AAQ94620 pTAR-PRE-	208	24	2.4	2434	7	ABQ77389	ABQ77389 Human AMP
136	24	2.4	448	3	AAc97748	AAc97748 Bridge-1	209	24	2.4	2480	4	AAAD06509	AAAD06509 Human CON
137	24	2.4	465	6	ABN94845	ABN94845 Gene #134	210	24	2.4	2538	6	AAAD21883	AAAD21883 Human TM4
138	24	2.4	474	2	AAQ03413	AAQ03413 Nucleotid	211	24	2.4	2700	8	AAI62308	AAI62308 Soybean c
139	24	2.4	486	7	ABZ73042	ABZ73042 Rice leaf	212	24	2.4	3213	2	AAV55742	AAV55742 Human sec
140	24	2.4	489	7	ACC60406	ACC60406 Rice leaf	213	24	2.4	3213	6	ABQ92068	ABQ92068 Human pol
141	24	2.4	515	5	ABV13318	ABV13318 Human pro	214	24	2.4	3360	4	ABL26030	ABL26030 Drosophil
142	24	2.4	516	5	ABV13318	ABV13318 Human pro	215	24	2.4	4074	6	ABT199626	ABT199626 Mouse isc
143	24	2.4	521	6	ABX54955	ABX54955 Human col	216	24	2.4	4074	6	ABQ74268	ABQ74268 Human 670
144	24	2.4	526	7	ABX98473	ABX98473 Rice albu	217	24	2.4	4582	9	ABD37486	ABD37486 Human tra
145	24	2.4	527	7	ACC55423	ACC55423 Rice endo	218	24	2.4	1388	4	ABL05670	ABL05670 Drosophil
146	24	2.4	535	5	ABV48043	ABV48043 Human pro	219	24	2.4	18011	6	ABL32034	ABL32034 Human imm
147	24	2.4	545	5	ABX98574	ABX98574 Rice leaf	220	24	2.4	50000	3	AAAG6363	AAAG6363 Polymorph
148	24	2.4	578	2	AAQ67607	AAQ67607 PV3TA-LTR	221	24	2.4	90220	4	ABK83576	ABK83576 Human cDN
149	24	2.4	595	3	AAAL6271	AAAL6271 Human col	222	24	2.4	40	4	AAH20341	AAH20341 HRV6 viru
150	24	2.4	604	7	ABX78368	ABX78368 Wheat str	223	23	2.3	51	4	AAI30739	AAI30739 Human SNP
151	24	2.4	637	4	AAAL15507	AAAL15507 Human bre	224	23	2.3	51	4	AAI32426	AAI32426 Human SNP
152	24	2.4	662	6	ABQ57172	ABQ57172 Human col	225	23	2.3	51	4	AAI27842	AAI27842 Human SNP
153	24	2.4	685	6	AAAL37825	AAAL37825 Rice KCP-	226	23	2.3	114	4	AAK55505	AAK55505 Human imm
154	24	2.4	690	7	ACA04882	ACA04882 Rice cDNA	227	23	2.3	119	6	ABV96775	ABV96775 Human pan
155	24	2.4	692	2	AAV65762	AAV65762 Pathogen	228	23	2.3	121	6	ABK25162	ABK25162 Male-ster
156	24	2.4	695	8	ADA21181	ADA21181 Human sec	229	23	2.3	121	6	ABK25161	ABK25161 Male-ster
157	24	2.4	756	4	AAAL24351	AAAL24351 Human bre	230	23	2.3	130	4	AA556565	AA556565 Human cDN
158	24	2.4	765	3	AAc59300	AAc59300 Human sec	231	23	2.3	130	7	ABX50278	ABX50278 Bovine ES
159	24	2.4	784	9	ADe62179	ADe62179 Human gen	232	23	2.3	158	4	AAI34673	AAI34673 Human mus
160	24	2.4	802	4	AAI94794	AAI94794 Human neu	233	23	2.3	158	7	ABX57661	ABX57661 cDNA enco
161	24	2.4	817	2	AAZ16657	AAZ16657 Human neu	234	23	2.3	159	4	AAK56708	AAK56708 Human imm
162	24	2.4	890	3	AAZ50159	AAZ50159 Corn Aden	235	23	2.3	161	6	ABL86196	ABL86196 Human ova
163	24	2.4	898	4	AAAS33229	AAAS33229 DNA encod	236	23	2.3	202	6	ABL85969	ABL85969 Human ova
164	24	2.4	923	2	AAV04582	AAV04582 Flea seri	237	23	2.3	203	7	ABZ49827	ABZ49827 Bovine ES
165	24	2.4	1004	6	AAH78831	AAH78831 Human rib	238	23	2.3	270	7	ABX72981	ABX72981 Rice leaf
166	24	2.4	1004	6	AAI5495	AAI5495 DNA encod	239	23	2.3	275	2	AAQ60278	AAQ60278 Human bra
167	24	2.4	1004	8	ACD27686	ACD27686 Human cDN	240	23	2.3	276	6	ABL86284	ABL86284 Human ova
168	24	2.4	1079	9	ADD48673	ADD48673 Human gen	241	23	2.3	276	6	ACC60351	ACC60351 Rice leaf
169	24	2.4	1093	3	AAc59720	AAc59720 Human sec	242	23	2.3	284	5	ABV38207	ABV38207 Human pro

243	23	2.3	288	6	ABQ57354	Human col	316	2.3	519	6	ABQ24717	Oligonucle
244	23	2.3	289	6	ABL87876	Human, enco	317	2.3	519	6	ABK54880	Human col
245	23	2.3	291	6	ABK44641	CDNA, ova	318	2.3	521	5	AAS09044	Human MEK
246	23	2.3	295	6	ABK46022	CDNA, enco	319	2.3	530	5	ABV61705	Human pro
247	23	2.3	286	6	ABV97630	Human pan	320	2.3	531	5	ABV49683	Human pro
248	23	2.3	300	6	ABL82272	Human ova	321	2.3	531	6	ABL38044	Human col
249	23	2.3	301	8	ACH34179	Human end	322	2.3	533	6	ABQ58979	Human col
250	23	2.3	308	3	AAC97730	Bridge-1	323	2.3	534	7	ACA10307	Rice leaf
251	23	2.3	309	5	ABV49040	Human pro	324	2.3	535	7	ABZ73036	Rice leaf
252	23	2.3	314	3	ACH97752	Bridge-1	325	2.3	537	6	ABV96144	Human pan
253	23	2.3	314	3	AAC97733	Bridge-1	326	2.3	544	7	ACC60103	Rice leaf
254	23	2.3	317	5	ABV58492	Human pro	327	2.3	545	3	AZ80422	Human col
255	23	2.3	316	6	ABL65547	Lung canc	328	2.3	576	7	ABX61460	Arabidops
256	23	2.3	317	6	ABL66019	Lung canc	329	2.3	576	7	ABX56870	Arabidops
257	23	2.3	319	7	ABX49797	Bovine ES	330	2.3	589	4	AAH10768	Human CDN
258	23	2.3	321	3	AAA770159	Plasmodiu	331	2.3	590	4	AAK58428	Human imm
259	23	2.3	325	6	ABL77085	Human ova	332	2.3	602	6	ABQ30024	Oligonucle
260	23	2.3	329	8	ACH32550	Human end	333	2.3	602	6	ABQ30025	Oligonucle
261	23	2.3	332	7	ABX46789	Bovine ES	334	2.3	602	6	ABN73413	Bovine em
262	23	2.3	338	5	ABV37757	Human pro	335	2.3	623	6	ABQ52237	Oligonucle
263	23	2.3	363	5	ABV07659	Human pro	336	2.3	623	6	ABQ52236	Oligonucle
264	23	2.3	364	6	AAS61750	Lung smal	337	2.3	627	6	ABQ52242	Oligonucle
265	23	2.3	364	9	ADD66939	Human lun	338	2.3	627	6	ABQ52243	Oligonucle
266	23	2.3	364	9	AD88193	Human lun	339	2.3	630	6	ABZ15972	Arabidops
267	23	2.3	369	7	ACH93828	Cat flea	340	2.3	630	6	ABZ15156	Arabidops
268	23	2.3	369	7	ABX35859	Bovine ES	341	2.3	636	6	ABQ42937	Oligonucle
269	23	2.3	376	7	ACC55387	Rice endo	342	2.3	636	6	ABQ42936	Oligonucle
270	23	2.3	380	8	ACH35080	Human end	343	2.3	646	6	ABQ66002	Arabidops
271	23	2.3	400	4	AAS60291	Human can	344	2.3	658	3	AAC59128	Human sec
272	23	2.3	403	6	ABQ58394	Human col	345	2.3	678	6	ABQ60251	Human col
273	23	2.3	404	5	AAF67426	Novel hum	346	2.3	681	4	AAF85393	Nucleotid
274	23	2.3	413	7	ABX62416	Arabidops	347	2.3	712	3	AAC64050	Trypanoso
275	23	2.3	418	5	ABV49108	Human pro	348	2.3	712	3	AAC64050	Trypanoso
276	23	2.3	418	7	ABX62296	Arabidops	349	2.3	744	3	AAF95537	Human sec
277	23	2.3	419	5	AAH88021	Peppermin	350	2.3	764	3	AAF21707	Human bre
278	23	2.3	422	4	AAI62566	Human rep	351	2.3	772	4	ABL24956	Human bre
279	23	2.3	422	4	AAI02612	Human rep	352	2.3	786	6	ABQ33463	Oligonucle
280	23	2.3	422	5	ABAI3982							

C 535	23	2.3	14708	6	ABL34245	ABL34245 Human imm	C 608	109	5	AAF98685	Aaf98685 Human ova
C 536	23	2.3	14708	6	ABL92325	ABL92325 Chemically	C 609	110	7	ABX53939	Abx53939 Bovine ES
C 537	23	2.3	14708	6	ABK28450	ABK28450 DNA trans	C 610	111	4	AA507743	AA507743 Cervical
C 538	23	2.3	15811	4	ABL112090	ABL112090 Drosophila	C 611	112	5	AH82332	Ah82332 Rat diffe
C 539	23	2.3	15863	9	ABD54166	ABD54166 Pretreat	C 612	113	7	ABX54764	Abx54764 Bovine ES
C 540	23	2.3	15954	6	ABK31494	ABK31494 Signal tr	C 613	114	6	ABV97532	Abv97532 Human pan
C 541	23	2.3	15954	6	ABL70467	ABL70467 Chemically	C 614	115	6	AAI19706	Aai19706 Human bre
C 542	23	2.3	17213	6	ABL33483	ABL33483 Human imm	C 615	116	4	AAF98629	Aaf98629 Human ova
C 543	23	2.3	49999	2	Az223895	Az223895 Murine LO	C 616	117	5	ABV33217	Abv33217 Human pro
C 544	23	2.3	72928	3	AAZ18355	AAZ18355 Human AST	C 617	118	5	ABV42140	Abv42140 Human pro
C 545	23	2.3	72928	3	AAA80253	AAA80253 Human AST	C 618	119	7	ABX48784	Abx48784 Bovine ES
C 546	23	2.3	73308	6	ABL66966	ABL66966 Lung canc	C 619	120	4	AAI00084	Aai00084 Human rep
C 547	23	2.3	93483	8	ADA03083	ADA03083 Mouse mCG	C 620	121	4	ABL96347	AbL96347 Human tes
C 548	23	2.3	93483	8	ADA66367	ADA66367 Mouse mCG	C 621	122	6	ABK25158	Abk25158 Male-ster
C 549	23	2.3	93483	9	ADB72821	ADB72821 Mouse mCG	C 622	123	6	ABK25157	Abk25157 Male-ster
C 550	22	2.2	2	2	ABX79828	ABX79828 EST polym	C 623	124	5	ABV61528	Abv61528 Mouse mit
C 551	22	2.2	30	6	ABX89953	ABX89953 PolyA ada	C 624	125	9	ADP35055	Adp35055 Mouse ova
C 552	22	2.2	35	6	ABS64697	ABS64697 Nucleic a	C 625	126	6	ABL86533	AbL86533 Bovine ES
C 553	22	2.2	35	7	AAV12343	AAV12343 Ribonucle	C 626	127	7	ABX54089	Abx54089 Bovine ES
C 554	22	2.2	37	3	AAZ43892	AAZ43892 M. tuberc	C 627	128	7	ABX60674	Abx60674 Arabidops
C 555	22	2.2	38	4	AAH20359	AAH20359 HIV6 viru	C 628	129	3	AAZ46504	Aaz46504 Mouse exo
C 556	22	2.2	39	4	ACC83851	ACC83851 Target-sp	C 629	130	4	AAZ46504	Aaz46504 Mouse exo
C 557	22	2.2	40	8	ACC83851	ACC83851 Human neu	C 630	131	6	ABK4612	Abk4612 Human ben
C 558	22	2.2	41	2	AAZ43851	AAZ43851 Primer fo	C 631	132	6	ABK4612	Abk4612 Human ben
C 559	22	2.2	41	2	AAZ43851	AAZ43851 Human SNP	C 632	133	9	ADP35055	Adp35055 Mouse ova
C 560	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 633	134	6	ABX54089	Abx54089 Bovine ES
C 561	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 634	135	7	ABX60674	Abx60674 Arabidops
C 562	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 635	136	7	ABX60674	Abx60674 Arabidops
C 563	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 636	137	7	ABX60674	Abx60674 Arabidops
C 564	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 637	138	7	ABX60674	Abx60674 Arabidops
C 565	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 638	139	7	ABX60674	Abx60674 Arabidops
C 566	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 639	140	7	ABX60674	Abx60674 Arabidops
C 567	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 640	141	7	ABX60674	Abx60674 Arabidops
C 568	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 641	142	7	ABX60674	Abx60674 Arabidops
C 569	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 642	143	7	ABX60674	Abx60674 Arabidops
C 570	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 643	144	7	ABX60674	Abx60674 Arabidops
C 571	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 644	145	7	ABX60674	Abx60674 Arabidops
C 572	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 645	146	7	ABX60674	Abx60674 Arabidops
C 573	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 646	147	7	ABX60674	Abx60674 Arabidops
C 574	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 647	148	7	ABX60674	Abx60674 Arabidops
C 575	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 648	149	7	ABX60674	Abx60674 Arabidops
C 576	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 649	150	7	ABX60674	Abx60674 Arabidops
C 577	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 650	151	7	ABX60674	Abx60674 Arabidops
C 578	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 651	152	7	ABX60674	Abx60674 Arabidops
C 579	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 652	153	7	ABX60674	Abx60674 Arabidops
C 580	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 653	154	7	ABX60674	Abx60674 Arabidops
C 581	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 654	155	7	ABX60674	Abx60674 Arabidops
C 582	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 655	156	7	ABX60674	Abx60674 Arabidops
C 583	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 656	157	7	ABX60674	Abx60674 Arabidops
C 584	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 657	158	7	ABX60674	Abx60674 Arabidops
C 585	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 658	159	7	ABX60674	Abx60674 Arabidops
C 586	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 659	160	7	ABX60674	Abx60674 Arabidops
C 587	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 660	161	7	ABX60674	Abx60674 Arabidops
C 588	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 661	162	7	ABX60674	Abx60674 Arabidops
C 589	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 662	163	7	ABX60674	Abx60674 Arabidops
C 590	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 663	164	7	ABX60674	Abx60674 Arabidops
C 591	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 664	165	7	ABX60674	Abx60674 Arabidops
C 592	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 665	166	7	ABX60674	Abx60674 Arabidops
C 593	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 666	167	7	ABX60674	Abx60674 Arabidops
C 594	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 667	168	7	ABX60674	Abx60674 Arabidops
C 595	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 668	169	7	ABX60674	Abx60674 Arabidops
C 596	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 669	170	7	ABX60674	Abx60674 Arabidops
C 597	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 670	171	7	ABX60674	Abx60674 Arabidops
C 598	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 671	172	7	ABX60674	Abx60674 Arabidops
C 599	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 672	173	7	ABX60674	Abx60674 Arabidops
C 600	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 673	174	7	ABX60674	Abx60674 Arabidops
C 601	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 674	175	7	ABX60674	Abx60674 Arabidops
C 602	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 675	176	7	ABX60674	Abx60674 Arabidops
C 603	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 676	177	7	ABX60674	Abx60674 Arabidops
C 604	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 677	178	7	ABX60674	Abx60674 Arabidops
C 605	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 678	179	7	ABX60674	Abx60674 Arabidops
C 606	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 679	180	7	ABX60674	Abx60674 Arabidops
C 607	22	2.2	41	7	AAZ43851	AAZ43851 Human SNP	C 680	181	7	ABX60674	Abx60674 Arabidops

681	22	2.2	162	3	AAC55654	AAC55654 Human dif	C 754	22	2.2	210	6	ABZ08498	Abz08498 Human leu
682	22	2.2	162	8	ACD81646	ACD81646 Human des	755	22	2.2	210	7	ACC55398	Acc55398 Rice endo
683	22	2.2	165	5	AA998642	AA998642 Human ova	756	22	2.2	210	9	AD45507	Ad45507 Human car
684	22	2.2	166	4	AA69428	AA69428 Human cer	757	22	2.2	211	4	AAL11252	Aal11252 Human bre
685	22	2.2	166	4	AB47844	AB47844 Bovine ES	758	22	2.2	211	5	ABV61155	Abv61155 Human pro
686	22	2.2	169	5	ABV38823	ABV38823 Human pro	759	22	2.2	211	5	ABL66058	AbL66058 Human ova
687	22	2.2	171	4	AAL08166	AAL08166 Human bre	760	22	2.2	212	6	ABV57286	Abv57286 Human pro
688	22	2.2	171	5	ABV57330	ABV57330 Human pro	761	22	2.2	212	6	ABQ56323	Abq56323 Human col
689	22	2.2	173	5	ABV36084	ABV36084 Human pro	762	22	2.2	212	5	ABV19566	Abv19566 Human pro
690	22	2.2	174	5	ABV37373	ABV37373 Human pro	763	22	2.2	213	5	ABV58569	Abv58569 Human pro
691	22	2.2	174	6	AB186789	AB186789 Human ova	764	22	2.2	214	7	ABX42742	Abx42742 Bovine ES
692	22	2.2	174	6	ABK55280	ABK55280 Human col	765	22	2.2	214	7	ABX39928	Abx39928 Bovine ES
693	22	2.2	174	6	ABV98545	ABV98545 Human pan	766	22	2.2	215	7	AAL10036	Aal10036 Human bre
694	22	2.2	176	5	ABV38031	ABV38031 Human pro	767	22	2.2	216	4	ABX46534	Abx46534 Bovine ES
695	22	2.2	177	4	AAI29159	AAI29159 Colon tum	768	22	2.2	217	5	ABV07377	Abv07377 Human pro
696	22	2.2	177	5	ABV56957	ABV56957 Human pro	769	22	2.2	218	5	ABX61564	Abx61564 Human pro
697	22	2.2	177	5	ABV35331	ABV35331 Human pro	770	22	2.2	218	7	ABX43361	Abx43361 Bovine ES
698	22	2.2	177	7	ABZ33345	ABZ33345 Human col	771	22	2.2	219	5	ABV44177	Abv44177 Human pro
699	22	2.2	178	4	AAL19616	AAL19616 Human bre	772	22	2.2	219	7	ABX39781	Abx39781 Bovine ES
700	22	2.2	178	5	ABV08201	ABV08201 Human pro	773	22	2.2	220	7	ABX49357	Abx49357 Bovine ES
701	22	2.2	178	7	ABT23025	ABT23025 Breast ca	774	22	2.2	220	7	ABV51803	Abv51803 Human pro
702	22	2.2	179	6	ABL86426	ABL86426 Human ova	775	22	2.2	221	7	ABX98463	Abx98463 Rice albu
703	22	2.2	181	7	ACC60155	ACC60155 Rice endo	776	22	2.2	222	4	AA60391	Aa60391 Human can
704	22	2.2	181	5	ABV54376	ABV54376 Human pro	777	22	2.2	222	5	ABV49733	Abv49733 Human pro
705	22	2.2	183	2	AAZ224556	AAZ224556 Bovine ES	778	22	2.2	222	6	ABX208197	Abx208197 Human leu
706	22	2.2	183	3	AAC65795	AAC65795 Human lun	779	22	2.2	222	5	AA184698	Aa184698 Human pol
707	22	2.2	183	6	ABL49014	ABL49014 Human lun	780	22	2.2	225	4	AA184698	Aa184698 Human pol
708	22	2.2	183	8	ABQ92200	ABQ92200 Human lun	781	22	2.2	225	5	AA184698	Aa184698 Human pol
709	22	2.2	183	9	ADA28615	ADA28615 Human lun	782	22	2.2	226	7	ACC60475	Acc60475 Rice leaf
710	22	2.2	184	5	ABV34425	ABV34425 Human lun	783	22	2.2	226	7	ABZ53968	Abz53968 Aspergill
711	22	2.2	184	5	ABV34425	ABV34425 Human lun	784	22	2.2	226	8	AAL60832	Aal60832 Human DNA
712	22	2.2	185	4	ACH21131	ACH21131 Human cer	785	22	2.2	227	5	ABV59030	Abv59030 Human pro
713	22	2.2	185	8	AAH70140	AAH70140 Human pro	786	22	2.2	228	7	ABX45169	Abx45169 Bovine ES
714	22	2.2	190	5	AAH08206	AAH08206 Human bre	787	22	2.2	228	7	ABX47094	Abx47094 Bovine ES
715	22	2.2	190	5	ABV56817	ABV56817 Human pro	788	22	2.2	229	5	ABV20080	Abv20080 Human pro
716	22	2.2	191	2	AAH13475	AAH13475 Capture p	789	22	2.2	229	5	ABV57465	Abv57465 Human pro
717	22	2.2	191	5	ABV04347	ABV04347 Human pro	790	22	2.2	230	5	ABV00395	Abv00395 Human pro
718	22	2.2	193	5	AAH83291	AAH83291 Human ova	791	22	2.2	230	5	AAH33958	Aah33958 Human col
719	22	2.2	195	4	AAH26235	AAH26235 Human bre	792	22	2.2	232	4	ABV30740	Abv30740 Human pro
720	22	2.2	195	5	ABV30808	ABV30808 Human pro	793	22	2.2	232	5	ABV58523	Abv58523 Human pro
721	22	2.2	196	6	ABL86047	ABL86047 Human ova	794	22	2.2	232	5	ABV58523	Abv58523 Human pro
722	22	2.2	199	4	AAL13185	AAL13185 Human bre	795	22	2.2	232	5	ABV07534	Abv07534 Human pro
723	22	2.2	199	6	ABO5451	ABO5451 Human col	796	22	2.2	232	6	ABK44812	Abk44812 cDNA enco
724	22	2.2	199	6	ABV35151	ABV35151 Bovine ES	797	22	2.2	233	3	AA433997	Aa433997 Mouse sec
725	22	2.2	200	7	ABX19076	ABX19076 Human pro	798	22	2.2	234	6	ABL67177	AbL67177 Thyroid c
726	22	2.2	200	7	ABZ49417	ABZ49417 Bovine ES	799	22	2.2	234	6	ABZ18079	Abz18079 S2 subtra
727	22	2.2	202	4	AAK78762	AAK78762 Human imm	800	22	2.2	235	7	ACF56930	Acf56930 Rice leaf
728	22	2.2	202	4	AAK84668	AAK84668 Human imm	801	22	2.2	235	7	ACF56930	Acf56930 Rice leaf
729	22	2.2	202	4	AAK79575	AAK79575 Human imm	802	22	2.2	236	3	ACC60486	Acc60486 Rice leaf
730	22	2.2	202	4	AAK79575	AAK79575 Human imm	803	22	2.2	236	3	AACT79014	Aac79014 Human sec
731	22	2.2	202	4	AAK79575	AAK79575 Human imm	804	22	2.2	236	3	AACT79014	Aac79014 Human sec
732	22	2.2	202	6	ABS68311	ABS68311 Genomic s	805	22	2.2	236	5	ABV56953	Abv56953 Human pro
733	22	2.2	202	7	ADA57786	ADA57786 BAC fragm	806	22	2.2	236	6	ABL66929	AbL66929 Lung canc
734	22	2.2	202	7	ABZ68127	ABZ68127 Human sec	807	22	2.2	236	6	ABV97471	Abv97471 Human pan
735	22	2.2	202	7	ABZ74606	ABZ74606 Secreted	808	22	2.2	237	5	ABV07534	Abv07534 Human pro
736	22	2.2	202	7	ADA41654	ADA41654 Human sec	809	22	2.2	237	7	ACC55510	Acc55510 Rice endo
737	22	2.2	202	7	ADA98983	ADA98983 Human sec	810	22	2.2	237	7	ACC55510	Acc55510 Rice endo
738	22	2.2	202	7	ABX47342	ABX47342 Bovine ES	811	22	2.2	237	7	ABX49378	Abx49378 Bovine ES
739	22	2.2	202	7	ABX3949	ABX3949 Bovine ES	812	22	2.2	239	5	ABAL1191	Abal1191 Human ner
740	22	2.2	202	9	ADC25433	ADC25433 Human cDN	813	22	2.2	239	5	ABV56818	Abv56818 Human pro
741	22	2.2	202	9	ADC74712	ADC74712 Human sec	814	22	2.2	240	5	ABV58851	Abv58851 Human pro
742	22	2.2	203	5	ABV56674	ABV56674 Human pro	815	22	2.2	240	5	ABV06841	Abv06841 Human pro
743	22	2.2	203	6	ABL85760	ABL85760 Human ova	816	22	2.2	241	7	ABX42739	Abx42739 Bovine ES
744	22	2.2	204	6	ABV97520	ABV97520 Human pan	817	22	2.2	242	7	ABX38052	Abx38052 Bovine ES
745	22	2.2	206	6	ABL86453	ABL86453 Human ova	818	22	2.2	242	7	ABX44816	Abx44816 Bovine ES
746	22	2.2	207	4	AAH71190	AAH71190 Human cer	819	22	2.2	243	4	AAL16042	Aal16042 Human bre
747	22	2.2	207	6	ABV97596	ABV97596 Human pan	820	22	2.2	244	3	AACT78309	Aac78309 Human can
748	22	2.2	208	4	AAS60654	AAS60654 Human can	821	22	2.2	244	4	AAL18637	Aal18637 Human bre
749	22	2.2	209	5	ABV07955	ABV07955 Human ova	822	22	2.2	244	6	ABV97987	Abv97987 Human pan
750	22	2.2	209	6	ABL86294	ABL86294 Human ova	823	22	2.2	245	5	ABV61393	Abv61393 Bovine ES
751	22	2.2	210	4	AAL19987	AAL19987 Human car	824	22	2.2	245	7	ABX42656	Abx42656 Bovine ES
752	22	2.2	210	4	AAS35428	AAS35428 Human car	825	22	2.2	245	7	ABX48909	Abx48909 Bovine ES
753	22	2.2	210	4	AAS35428	AAS35428 Human car	826	22	2.2	245	5	ABV19844	Abv19844 Human pro

CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

XX Sequence 121 BP; 20 A; 36 C; 40 G; 25 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 6; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ACCAACAGGCGAGTACTTCTCCAAAG 69

DB 106 ACCAACAGGCGAGTACTTCTCCAAAG 80

RESULT 4

ID ABK25241 standard; DNA; 121 BP.

XX AC ABK25241;

DT 09-APR-2002 (first entry)

DE Male-sterile plant producing genome altering oligonucleotide #141.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW increased stearate production; reduced palmitate production; albino plant;
 KW photosynthetic process.

XX Triticum aestivum.

OS Synthetic.

XX WO200192512-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

XX 27-MAR-2001; 2001US-00818975.

PA (UYDE) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful for

PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.

XX Claim 7; Page 79; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

SQ Sequence 121 BP; 25 A; 40 C; 36 G; 20 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 6; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ACCAACAGGCGAGTACTTCTCCAAAG 69

DB 16 ACCAACAGGCGAGTACTTCTCCAAAG 42

RESULT 5

ABK25237

ID ABK25237 standard; DNA; 121 BP.

XX AC ABK25237;

DT 09-APR-2002 (first entry)

DE Male-sterile plant producing genome altering oligonucleotide #137.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW increased stearate production; reduced palmitate production; albino plant;
 KW photosynthetic process.

OS Triticum aestivum.

OS Synthetic.

XX WO200192512-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

```
PR 30-OCT-2000; 2000US-0244989P.
XX 27-MAR-2001; 2001US-00818875.
XX (UYDE ) UNIV DELAWARE.
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
XX creating plants with desired phenotypes, e.g. stress tolerance, improved
XX nutritional value, herbicide or disease resistance, or modified oil
XX production.
XX Claim 7; Page 79; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
XX genetic sequence, which comprises a single-stranded oligonucleotide
XX having a DNA domain. The DNA domain has at least one mismatch with
XX respect to the genetic sequence to be altered and further comprises
XX chemical modifications of the oligonucleotide. The chemical modifications
XX consist of o-methyl modification, an LNA modification, two or more
XX phosphorothioate linkages on a terminus, or a combination of any two or
XX more of these modifications. The oligonucleotides are useful for
XX directing repair or alteration of plant genetic information. The
XX oligonucleotides are particularly useful for creating plants with desired
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved
XX nutritional value (e.g. altering amino acid content of plants or
XX conferring amino acid over production), herbicide resistance (e.g.
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide
XX resistance, porphyrin herbicide resistance or triazine resistance),
XX disease resistance, modified oil production, modified starch production
XX (e.g. increased starch or production of waxy starch), altered floral
XX morphology (e.g. male-sterile plants) or modified fatty acid content
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
XX The oligonucleotides are also useful for producing albino mutants for the
XX analysis of photosynthetic processes. This sequence represents a genome
XX altering oligonucleotide of the invention
XX
XX Sequence 121 BP; 31 A; 35 C; 38 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 27; DB 6; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.36;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 43 ACCAACAGGCGAGTGACCTACTCCAAAG 69
XX |||||
XX Db 27 ACCAACAGGCGAGTGACCTACTCCAAAG 53
XX
XX RESULT 6
XX ABK25238/C
XX -ID ABK25238 standard; DNA; 121 BP.
XX
XX AC ABK25238;
XX
XX XX 09-APR-2002 (first entry)
XX
XX DE Male-sterile plant producing genome altering oligonucleotide #138.
XX
XX KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
XX o-methyl modification; LNA modification; phosphorothioate linkage;
XX DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
XX abiotic stress tolerance; improved nutritional value; hygromycin-B;
XX amino acid over production; herbicide resistance; glyphosate resistance;
XX imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
XX porphyrin herbicide resistance; triazine resistance; disease resistance;
XX modified oil production; modified starch production; waxy starch;
XX altered floral morphology; male-sterile plant; albino mutant;
XX modified fatty acid content; reduced palmitate production; albino plant;
XX increased stearate production; reduced linolenic acid production;
XX photosynthetic process.
XX
OS Triticum aestivum.
XX Synthetic.
XX W0200192512-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 01-JUN-2001; 2001WO-US017672.
XX
XX PR 01-JUN-2000; 2000US-0208538P.
XX 30-OCT-2000; 2000US-0244989P.
XX 27-MAR-2001; 2001US-00818875.
XX
XX PA (UYDE ) UNIV DELAWARE.
XX
XX PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX DR New oligonucleotides with modified nuclease-resistant termini, useful for
XX creating plants with desired phenotypes, e.g. stress tolerance, improved
XX nutritional value, herbicide or disease resistance, or modified oil
XX production.
XX Claim 7; Page 79; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
XX genetic sequence, which comprises a single-stranded oligonucleotide
XX having a DNA domain. The DNA domain has at least one mismatch with
XX respect to the genetic sequence to be altered and further comprises
XX chemical modifications of the oligonucleotide. The chemical modifications
XX consist of o-methyl modification, an LNA modification, two or more
XX phosphorothioate linkages on a terminus, or a combination of any two or
XX more of these modifications. The oligonucleotides are useful for
XX directing repair or alteration of plant genetic information. The
XX oligonucleotides are particularly useful for creating plants with desired
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved
XX nutritional value (e.g. altering amino acid content of plants or
XX conferring amino acid over production), herbicide resistance (e.g.
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide
XX resistance, porphyrin herbicide resistance or triazine resistance),
XX disease resistance, modified oil production, modified starch production
XX (e.g. increased starch or production of waxy starch), altered floral
XX morphology (e.g. male-sterile plants) or modified fatty acid content
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
XX The oligonucleotides are also useful for producing albino mutants for the
XX analysis of photosynthetic processes. This sequence represents a genome
XX altering oligonucleotide of the invention
XX
XX Sequence 121 BP; 17 A; 38 C; 35 G; 31 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 27; DB 6; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.36;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 43 ACCAACAGGCGAGTGACCTACTCCAAAG 69
XX |||||
XX Db 95 ACCAACAGGCGAGTGACCTACTCCAAAG 69
XX
XX RESULT 7
XX ACH38095
XX -ID ACH38095 standard; cDNA; 390 BP.
XX
XX AC ACH38095;
XX
XX DT 13-OCT-2003 (first entry)
XX
XX DE Human endothelial cell cDNA #6228.
XX
XX KW Human; ss; sequencing by hybridisation; SH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
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OS Homo sapiens.
 XX US2003073623-A1.
 XX PD 17-APR-2003.
 XX 30-JUL-2001; 2001US-00918995.
 XX PR 30-JUL-2001; 2001US-00918995.
 XX (DRNA/) DRMANAC R T.
 XX (LABA/) LABAT I.
 XX (STAC/) STACHE-CRAIN B.
 XX (DICK/) DICKSON M C.
 XX (JONE/) JONES L W.
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 PI WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX Claim 1; SEQ ID NO 25307; 44pp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX Sequence 390 BP; 91 A; 131 C; 97 G; 65 T; 0 U; 6 Other;
 SQ Query Match 2.7%; Score 27; DB 8; Length 390;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 982
 DB 363 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 389
 RESULT 8
 ABL93709/c
 ID ABL93709 standard; DNA; 448 BP.
 XX ABL93709;
 AC ABL93709;
 XX 26-FEB-2003 (first entry)
 DT Arabidopsis thaliana polynucleotide #249.
 XX Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;
 KW genetic modification; environmental stress; disease resistance;
 KW fungicide; insecticide; stress tolerance.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX Arabidopsis thaliana nucleic acid sequence Ref:2027474 SEQ ID NO:474.
 XX US2002142319-A1.

XX 03-OCT-2002.
 XX 07-AUG-2001; 2001US-00924035.
 XX 13-AUG-1999; 99US-0148784P.
 XX 11-AUG-2000; 2000US-00638258.
 XX (GORL/) GORLACH J.
 XX (ANTI/) AN Y.
 XX (HAMI/) HAMILTON C M.
 XX (PRIC/) PRICE J L.
 XX (HARG/) HARGISS T R.
 XX (YUYV/) YU Y.
 XX (RAME/) RAMEAKA J G.
 XX (PAGE/) PAGE A.
 XX (MATH/) MATHAW A V.
 XX (LEDF/) LEDFORD B L.
 XX (WOES/) WOESSNER J P.
 XX (HAAS/) HAAS W D.
 XX (GARC/) GARCIA C A.
 XX Gorlach J, An Y, Hamilton CM, Price JL, Hargiss TR, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA;
 XX WPI; 2003-102509/09.
 XX Novel Arabidopsis thaliana nucleic acid useful for constructing a
 PT transgenic plant with enhanced disease resistance and enhanced traits of
 PT interest, as probes, and in diagnosis and screening purposes.
 XX Claim 1; Page 86; 277pp; English.
 XX The invention relates to Arabidopsis thaliana nucleic acid sequences. The
 CC DNA sequences and the polypeptides they encode are useful for identifying
 CC homologous or related genes, for producing compositions that modulate the
 CC expression or function of the polypeptides, for mapping functional
 CC regions of the protein, in diagnosis, for studying associated
 CC physiological pathways, for genetic manipulation of cells, preferably
 CC plant cells, in screening assays of various plant strains to determine
 CC the strains that are capable of withstanding a particular disease or
 CC environmental stress, for enhancing or inhibiting production of
 CC biosynthetic products in plants and to create genetically modified and
 CC transgenic organisms, such as plant cells and plants. Transgenic plants
 CC are useful for introducing or improving disease resistance and stress
 CC tolerance in plants, screening biologically active agents, such as
 CC fungicides and insecticides, and for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial or medicinal value.
 CC Sequences ABX0655-ABX61554 represent Arabidopsis thaliana
 CC polynucleotides of the invention
 XX SQ Sequence 448 BP; 118 A; 82 C; 85 G; 163 T; 0 U; 0 Other;
 Query Match 2.7%; Score 27; DB 7; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 982
 DB 57 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 31
 RESULT 9
 ABL93709/c
 ID ABL93709 standard; cDNA; 458 BP.
 XX ABL93709;
 AC ABL93709;
 XX 10-JUN-2002 (first entry)
 DT Arabidopsis thaliana nucleic acid sequence Ref:2027474 SEQ ID NO:474.
 XX Arabidopsis thaliana nucleic acid sequence Ref:2027474 SEQ ID NO:474.

KW Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;
KW Genetic modification; gene; ss.
OS Arabidopsis thaliana.
XX US2002023280-A1.
FN PD 21-FEB-2002.
XX PF 26-JAN-2001; 2001US-00770444.
XX PR 27-JAN-2000; 2000US-0178502P.
XX PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX WPI; 2002-267486/31.
XX New Arabidopsis thaliana nucleic acid, for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of a protein.
XX Claim 1; SEQ ID NO 474; 44pp; English.
XX The present invention describes an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridizing under stringent conditions
CC to a sequence (S1) selected from any one of the 999 sequences given in
CC ABL93236 to ABL94234. (I) have insecticide and fungicide activities, and
CC they can be used as protein expression modulators. (I) can be used in
CC identifying homologous or related genes, in producing compositions that
CC modulate the expression or function of their encoded proteins, mapping
CC functional regions of the proteins, and in studying associated
CC physiological pathways. (I) can also be used: (1) for the genetic
CC manipulation of cells, particularly plant cells; (2) in screening assays
CC of various plant strains to determine the strains that are best capable
CC of withstanding a particular disease or environmental stress; (3) for
CC enhancing or inhibiting production of a biosynthetic product in a plant;
CC (4) as probes in mapping and in diagnosis, in genetic modification and
CC for screening purposes, to generate additional copies of the nucleic
CC acids, to generate ribozymes or antisense oligonucleotides, and as single
CC -stranded DNA probes or as triple-strand forming oligonucleotides; and (5)
CC for generating genetically modified transgenic organisms. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site
XX SQ Sequence 458 BP; 131 A; 71 C; 74 G; 182 T; 0 U; 0 Other;
Query Match 2.7%; Score 27; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 982
DB 82 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 56

RESULT 10

ABQ65619/C
ID ABQ65619 standard; DNA; 712 BP.

XX AC ABQ65619;
XX DT 21-AUG-2002 (first entry)
XX DE Arabidopsis thaliana polynucleotide SEQ ID NO 196.

XX Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
KW stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
KW insecticide; antibiotic; ds.
XX OS Arabidopsis thaliana.

XX US2002059663-A1.

XX PD 16-MAY-2002.

XX PF 26-JAN-2001; 2001US-00770149.

XX PR 27-JAN-2000; 2000US-0178506P.

XX PA (GORL/) GORLACH J.

PA (ANY/) AN Y.

PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.

PA (RAIN/) RAINES T M.

PA (YUY/) YU Y.

PA (RAME/) RAMEAKA J G.

PA (PAGE/) PAGE A.

PA (MATH/) MATHW A V.

PA (LEDF/) LEDFORD B L.

PA (WOES/) WOESSNER J P.

PA (HAAS/) HAAS W D.

PA (GARC/) GARCIA C A.

PA (KRIC/) KRICKER M.

PA (SLAT/) SLATER T.

PA (DAVI/) DAVIS K R.

PA (ALLE/) ALLEN K.

PA (HOFF/) HOFFMAN N.

PA (HURB/) HURBAN P.

XX PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;

XX WPI; 2002-479224/51.

XX New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
PT useful e.g. for preparing transgenic plants with increased resistance or
PT altered metabolism.
XX Claim 1; SEQ ID NO 196; 40pp + Sequence Listing; English.

XX The invention relates to nucleic acids (I) that hybridize under stringent
CC conditions to any of 999 sequences (ABQ65424-ABQ66422) or their
CC fragments. (I) are used to express the corresponding polypeptides (II) or
CC to produce genetically modified plant cells or transgenic plants, which
CC may have improved resistance to disease or stress, or altered
CC metabolic/biosynthetic pathways (for production of commercial,
CC nutritional or medicinal products), or generally any trait of interest,
CC or can be used to screen for biologically active agents (e.g. fungicides,
CC insecticides and antibiotics). Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in

CC electronic format directly from the USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=99909770149

XX Sequence 712 BP; 198 A; 194 C; 132 G; 188 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 6; Length 712;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 955 CTTTGGATATAAAAAAAAAAAAAAAAAAAAA 981
 DB 28 CTTTGGATATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 11
 AAD06338
 ID AAD06338 standard; cDNA; 980 BP.

XX AAD06338;

DT 06-AUG-2003 (revised)

DT 10-AUG-2001 (first entry)

DE Pentaclethra macroloba partial lipid acyl hydrolase (LAH) cDNA.

KW Pentin-1; lipid acyl hydrolase; LAH; gene shuffling; insecticidal;
 KW pathogenic infection; pesticidal; transgenic plant; insect infestation;
 KW genetic manipulation; agricultural crop; ss.

OS Pentaclethra macroloba.

PH Key Location/Qualifiers
 FT CDS 1..828

FT /tag= a
 FT /product= "Lipid acyl hydrolase (LAH) protein"
 FT /note= "Does not include start codon"
 FT /partial

PN WO200136468-A2.

PD 25-MAY-2001.

PF 15-NOV-2000; 2000WO-US031408.

PR 15-NOV-1999; 99US-0165455P.

PA (PION-) PIONEER HI-BRED INT INC.

PI Cigan AL;

XX WPI; 2001-355613/37.

DR P-PSDB; AAE02392.

PT New nucleic acid encoding lipid acyl hydrolase proteins having pesticidal
 PT activity, derived from rice, soybean, or wheat, for controlling insect
 PT infestation and pathogenic infection in transgenic plants.

PS Claim 1; Fig 7; 89pp; English.

XX The invention relates to Pentin-1-like lipid acyl hydrolases (LAH) and
 CC their corresponding cDNA molecules. LAH is useful for controlling insect
 CC infestation and pathogenic infections in transgenic plants. LAH cDNA
 CC confers pesticidal resistance to organisms into which it has been
 CC introduced and is also useful in mutagenic and recombinogenic protocols,
 CC to produce polypeptides with improved biological activities. LAH cDNA is
 CC also useful in the genetic manipulation of plants and for transforming
 CC bacteria, fungi, yeast and other organisms. LAH having pesticidal
 CC activity is useful for protecting plants, in particular agricultural
 CC crops from pests, including insects, fungi, bacteria, nematodes, viruses
 CC or viroids and in particular insect pests. LAH cDNA is further useful in
 CC gene shuffling protocols for generating libraries of polynucleotides
 CC having a desired characteristic. LAH can be used alone or in combination
 CC with other proteins or agents from Bacillus, including delta-endotoxin

CC and vegetative insecticidal proteins, protease inhibitors, lectins, alpha
 CC -amylases, peroxidases and cholesterol oxidase, to control different
 CC insect pests. The present cDNA sequence encodes partial Pentaclethra
 CC lipid acyl hydrolase (LAH) protein. (Updated on 06-AUG-2003 to correct OS
 CC field.)

XX Sequence 980 BP; 341 A; 177 C; 197 G; 265 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 4; Length 980;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 954 GCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 980
 DB 954 GCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 980

RESULT 12

AAT66687

ID AAT66687 standard; cDNA; 1167 BP.

XX AAT66687;

DT 17-OCT-2003 (revised)

DT 25-JUL-1997 (first entry)

XX Soybean peroxidase SEPB2 cDNA.

KW Peroxidase; SEPB2; soybean; plant breeding; pulp; paper; bleaching;
 KW waste disposal; soil reclamation; remediation; monoclonal antibody; ss.

XX Glycine max; cv. Resnik.

PH Key Location/Qualifiers
 FT CDS 39..980

FT /tag= a

FT sig_peptide 39..101

FT /tag= b

FT mat_peptide 102..977

FT /tag= c

FT polyA_signal 1126..1130

FT /tag= d

PN WO9715656-A1.

XX 01-MAY-1997.

PF 11-OCT-1996; 96WO-US016354.

PR 27-OCT-1995; 95US-00549658.

PA (INDI-) INDIANA CROP IMPROVEMENT ASSOC.

PI Vierling RA;

XX WPI; 1997-259011/23.

DR P-PSDB; AAW16610.

PT Isolated soybean peroxidase genes - useful for developing products for
 PT quantification and monitoring of peroxidase activity.

PS Claim 16; Page 43-44; 63pp; English.

XX cDNA clones (AAT66684-87) respectively code for soybean peroxidases
 CC SEPA1, SEPB2, SEPB1 and SEPB2 (AAW16607-10). Plant peroxidase specific
 CC primer PSP (AAT66679) was generated from the conserved distal haem ligand
 CC (AAW16603) in all plant peroxidases, and was used to generate a
 CC peroxidase gene probe. Primary hybridisation screening using the probe
 CC yielded 25 clones. 11 Positive clones were recovered after 2 rounds of
 CC PCR using PSP and a T7 vector primer, and 4 clones, SEPA1, SEPB2, SEPB1
 CC and SEPB2, were further analysed. The soybean peroxidase genes can be
 CC used to develop products for the quantification and monitoring of
 CC peroxidase activity, e.g. in assays such as ELISA, PCR, plant breeding

CC programmes, pulp and paper bleaching, on-site waste destruction, soil
 CC remediation and organic synthesis. (Updated on 17-OCT-2003 to standardise
 CC OS field)

XX Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 2; Length 1167;

Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 982

Db 1139 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 1165

RESULT 13

AAV69276
 ID AAV69276 standard; cDNA; 1167 BP.

XX AC AAV69276;

XX DT 29-JAN-1999 (first entry)

XX DE Soybean peroxidase SEPB2 polypeptide encoding cDNA.

XX DE Soybean peroxidase; SEPal; SEPa2; SEPB1; SEPB2; recombinant; industry;
 KW diagnostic chemistry; ss.

XX OS Glycine max.

XX FH Key Location/Qualifiers

FT 5'UTR 1..38

FT /*tag= a

FT CDS 39..980

FT /*tag= b

FT /product= "SEPB2 polypeptide"

FT sig_peptide 39..101

FT /*tag= c

FT mat_peptide 102..977

FT /*tag= d

FT 3'UTR 978..1167

FT /*tag= e

XX PN US5840558-A.

XX XX 24-NOV-1998.

XX XX 27-OCT-1995;

XX PF 95US-00671320.

XX PR 27-OCT-1995;

XX PR 95US-00671320.

XX PA (INDI-) INDIANA CROP IMPROVEMENT ASSOC.

XX XX Vierling RA;

XX PI WPI; 1999-034041/03.

XX DR P-PSDB; AAW81496.

XX DR cDNA encoding soya peroxidase SEPal - useful for producing recombinant

XX PT peroxidase.

XX PS Example 7; Col 35-38; 31pp; English.

XX XX This cDNA encodes a soybean peroxidase SEPB2 polypeptide. The invention

XX CC provides four cDNA sequences (AAV69273 to AAV69276) encoding soybean

XX CC peroxidases SEPal, SEPa2, SEPB1 and SEPB2 (AAW81493 to AAW81496)

XX CC respectively. An expression vector containing the SEPal cDNA sequence can

XX CC be used to transform host cells for the recombinant production of the

XX CC peroxidase. The peroxidase is useful in industries and diagnostic

XX CC chemistries

XX XX Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;

XX SQ

Query Match 2.7%; Score 27; DB 2; Length 1167;

Best Local Similarity 100.0%; Pred. No. 0.26;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 982

Db 1139 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 1165

RESULT 14

AAV81423
 ID AAV81423 standard; cDNA; 1167 BP.

XX AC AAV81423;

XX DT 12-APR-1999 (first entry)

XX DE Soybean peroxidase SEPB2 cDNA.

XX DE Peroxidase; SEPB2; soybean; transgenic plant; immunoassay; assay; pulp;

KW paper; bleaching; bioremediation; soil decontamination; ss.

XX OS Glycine max.

XX FH Key Location/Qualifiers

FT CDS 39..980

FT /*tag= a

FT sig_peptide 39..101

FT /*tag= b

FT mat_peptide 102..977

FT /*tag= c

FT polyA_signal 1126..1131

FT /*tag= d

XX XX WO9855629-A2.

XX PN 10-DEC-1998.

XX PD 04-JUN-1998;

XX PF 98WO-US011421.

XX PR 04-JUN-1997;

XX PR 97US-00868577.

XX XX (INDI-) INDIANA CROP IMPROVEMENT ASSOC.

XX PA Vierling RA;

XX PI WPI; 1999-070273/06.

XX DR P-PSDB; AAW67734.

XX DR New soybean peroxidase genes - useful, e.g. in pulp and paper bleaching,

XX PT on site waste destruction and soil remediation.

XX XX Example 8; Page 48-49; 78pp; English.

XX PS This cDNA clone codes for novel soybean peroxidase SEPB2 (see AAW67734).

XX CC 4 Clones, designated SEPal, SEPa2, SEPB1 and SEPB2 (see AAV81420-23) were

XX CC isolated from a soybean cv. Resnick seedling cDNA library using a plant

XX CC peroxidase specific primer (see AAV81424) and 3'RACE. Genomic clones (see

XX CC AAV81418-19) for SEPal and SEPB1 were also obtained. The coding regions of

XX CC SEPal and SEPB2 exhibit 97% amino acid identity, and the coding regions of

XX CC SEPB1 and SEPB2 share 95% amino acid identity, and the coding regions of

XX CC SEPal and SEPB1 share 47% amino acid identity. The peroxidases are useful

XX CC in pulp and paper bleaching, on-site waste destruction, soil remediation,

XX CC organic synthesis and diagnostic chemistries. Soybean peroxidase has

XX CC advantages over chlorine bleach, being cheaper, more environmentally

XX CC friendly, and producing hydroxyl ions with twice the oxidising power of

XX CC chlorine ions. The plant enzyme is cheap and easy to produce. The

XX CC invention also relates to immunoassays or oligonucleotide assays which

XX CC utilise soybean peroxidase as marker

XX XX Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;

XX SQ

Query Match

2.7%; Score 27; DB 2; Length 1167;

	Best Local Similarity	100.0%; Pred. No.	0.26;	Mismatches	27; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
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XX	DT	06-NOV-2003	(first entry)						
XX	DE	cDNA encoding soybean peroxidase GmEPB2.							
XX	KW	Soybean peroxidase; gene promoter; transgenic plant; peroxidase activity;							
XX	KX	plant; GmEPB2; gene; ss.							
XX	OS	Glycine max.							
XX	FH	Key	Location/Qualifiers						
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FT	FT		/tag= a						
CDS	FT		39..980						
FT	FT		/tag= C						
FT	FT		/product= "GmEPB2"						
FT	FT	sigs_peptide	39..101						
FT	FT		/tag= b						
FT	FT	mat_peptide	102..977						
FT	FT		/tag= d						
FT	FT	3'UTR	981..1167						
FT	FT		/tag= e						
XX	FN	US6586583-B1.							
XX	PD	01-JUL-2003.							
XX	PJ	09-DEC-1998;	98US-00207914.						
PR	PT	27-OCT-1995;	95US-00671320.						
PR	PT	04-JUN-1997;	97US-00868577.						
XX	PA	(INDI-) INDIANA CROP IMPROVEMENT ASSOC.							
PI	PI	Vierling RA;							
DR	DR	WI; 2003-669569/63.							
XX	DR	P-FSDB; ADA01012.							
PT	PT	New recombinant DNA molecule, useful for producing transgenic plants,							
PT	PT	including transgenic soybeans and in immunoassays or oligonucleotide assays that utilize soybean peroxidase as a marker.							
PS	PS	Example 7; Col 61-64; 85pp; English.							
CC	CC	The present invention relates to soybean peroxidase genomic DNA and gene promoters for producing transgenic plants, including soybean transgenic plants. The invention also relates to immunoassays or oligonucleotide assays which employ soybean peroxidase as a marker for peroxidase activity. The present sequence encodes soybean peroxidase GmEPB2.							
XX	SQ	Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;							
				Query Match					
				Best Local Similarity 100.0%; Score 27; DB 8; Length 1167;					
				Mismatches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	956 TTTTGATAAAAA	AAAAAAAAAAAAAAAAAA	982 	DG	1139 TTTTGATAAAAA	AAAAAAAAAAAAAAAAAA	1165 		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 22:22:22 ; Search time 85.9913 Seconds
(without alignments)
6337.402 Million call updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgccgggaagattga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: OLIGO.NUC

Gapop 50.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents.NA.*

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- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	26	2.6	1154	3	US-08-651-136C-7
5	26	2.6	1154	4	US-09-229-911A-7
6	26	2.6	1378	6	5188642-3
7	25	2.5	396	4	US-09-640-173-77
8	25	2.5	396	4	US-09-713-550-77
9	25	2.5	1146	3	US-08-893-654B-5
10	25	2.5	1402	3	US-09-196-520-5
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13	25	2.5	4134	4	US-09-687-477-17
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21	24	2.4	64	1	US-08-055-390-10
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23	24	2.4	923	3	US-09-004-731-66
24	24	2.4	923	3	US-08-749-699-66
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32	24	2.4	1624	3	US-08-582-740-67	Sequence 67, Appli
33	24	2.4	1624	3	US-09-109-879-67	Sequence 67, Appli
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35	24	2.4	1921	4	US-09-057-996-7	Sequence 7, Appli
36	24	2.4	1971	2	US-08-892-770-4	Sequence 2, Appli
37	24	2.4	2187	4	US-09-127-219B-2	Sequence 22, Appli
38	23	2.3	40	3	US-09-306-290-22	Sequence 22, Appli
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834	21	2.1	372	4	US-08-300-958A-15	Sequence 15, Appl	907	21	2.1	437	4	US-09-221-107-74	Sequence 74, Appl
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845	21	2.1	391	4	US-09-621-976-18858	Sequence 18858, A	918	21	2.1	463	4	US-09-621-976-3677	Sequence 3677, Appl
846	21	2.1	393	4	US-09-439-313-357	Sequence 357, Appl	919	21	2.1	465	4	US-09-328-475C-132	Sequence 132, Appl
847	21	2.1	393	4	US-09-352-616A-357	Sequence 357, Appl	920	21	2.1	467	4	US-09-621-976-3668	Sequence 3668, Appl
848	21	2.1	393	4	US-09-636-155-357	Sequence 357, Appl	921	21	2.1	469	4	US-09-621-976-2632	Sequence 2632, Appl
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852	21	2.1	396	4	US-09-171-156A-33	Sequence 33, Appl	925	21	2.1	472	4	US-09-702-705-892	Sequence 892, Appl
853	21	2.1	396	4	US-09-004-730A-33	Sequence 33, Appl	926	21	2.1	472	4	US-09-736-457-892	Sequence 892, Appl
854	21	2.1	396	4	US-09-495-050A-98	Sequence 98, Appl	927	21	2.1	472	4	US-09-614-124B-892	Sequence 892, Appl
855	21	2.1	396	4	US-08-981-799A-33	Sequence 33, Appl	928	21	2.1	472	4	US-09-671-325-892	Sequence 892, Appl
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872	21	2.1	399	1	US-08-298-687A-13	Sequence 13, Appl	945	21	2.1	484	4	US-09-480-251-1	Sequence 1, Appl
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874	21	2.1	399	1	US-08-298-629-13	Sequence 13, Appl	947	21	2.1	489	4	US-08-630-822A-89	Sequence 89, Appl
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877	21	2.1	403	4	US-08-621-976-18962	Sequence 18962, A	950	21	2.1	493	4	US-09-004-730A-38	Sequence 38, Appl
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880	21	2.1	408	4	US-09-389-661-43	Sequence 43, Appl	953	21	2.1	496	4	US-08-904-615-60	Sequence 60, Appl
881	21	2.1	408	4	US-09-620-405B-43	Sequence 43, Appl	954	21	2.1	497	3	US-08-050-259B-17	Sequence 17, Appl
882	21	2.1	408	4	US-09-339-338-43	Sequence 43, Appl	955	21	2.1	500	4	US-09-833-381-514	Sequence 514, Appl
883	21	2.1	408	4	US-09-433-826B-43	Sequence 43, Appl	956	21	2.1	502	4	US-09-186-276B-29	Sequence 29, Appl
884	21	2.1	408	4	US-08-604-287A-43	Sequence 43, Appl	957	21	2.1	502	4	US-08-842-445-29	Sequence 29, Appl
885	21	2.1	408	4	US-08-285-480-43	Sequence 43, Appl	958	21	2.1	502	4	US-09-186-188B-29	Sequence 29, Appl
886	21	2.1	408	4	US-08-834-759-43	Sequence 43, Appl	959	21	2.1	506	3	US-09-328-111-746	Sequence 746, Appl
887	21	2.1	413	2	US-09-014-969-5	Sequence 5, Appl	960	21	2.1	506	4	US-09-442-631-1	Sequence 1, Appl
888	21	2.1	413	4	US-08-621-976-16710	Sequence 16710, A	961	21	2.1	506	4	US-09-370-838-263	Sequence 263, Appl
889	21	2.1	422	4	US-08-764-325A-3	Sequence 3, Appl	962	21	2.1	511	4	US-09-328-475C-196	Sequence 196, Appl
890	21	2.1	422	4	US-09-912-935-3	Sequence 3, Appl	963	21	2.1	515	4	US-09-130-158A-3	Sequence 3, Appl
891	21	2.1	424	4	US-08-621-976-11043	Sequence 11043, A	964	21	2.1	518	4	US-09-621-976-18356	Sequence 18356, A
892	21	2.1	425	4	US-08-621-976-16712	Sequence 16712, A	965	21	2.1	519	4	US-09-227-357-76	Sequence 76, Appl
893	21	2.1	427	4	US-09-091-097-41	Sequence 41, Appl	966	21	2.1	519	4	US-09-615-192A-364	Sequence 364, Appl
894	21	2.1	430	4	US-08-621-976-16711	Sequence 16711, A	967	21	2.1	522	2	US-08-909-965C-16	Sequence 16, Appl
895	21	2.1	435	3	US-09-385-982-518	Sequence 518, Appl	968	21	2.1	523	2	US-08-828-413-1	Sequence 1, Appl
896	21	2.1	436	4	US-09-439-313-353	Sequence 353, Appl	969	21	2.1	526	1	US-08-289-447B-2	Sequence 2, Appl
897	21	2.1	436	4	US-09-352-616A-353	Sequence 353, Appl	970	21	2.1	526	5	PCT-US95-09763-2	Sequence 2, Appl
898	21	2.1	436	4	US-09-636-215-353	Sequence 353, Appl	971	21	2.1	530	1	US-08-462-894-5	Sequence 5, Appl
899	21	2.1	436	4	US-08-688-166A-353	Sequence 353, Appl	972	21	2.1	530	1	US-08-206-185-5	Sequence 5, Appl
900	21	2.1	437	3	US-08-040-984-74	Sequence 74, Appl	973	21	2.1	530	4	US-09-461-325-28	Sequence 28, Appl
901	21	2.1	437	4	US-09-123-912-74	Sequence 74, Appl	974	21	2.1	530	4	US-10-012-542-28	Sequence 28, Appl
902	21	2.1	437	4	US-09-643-537-74	Sequence 74, Appl	975	21	2.1	536	3	US-09-040-584-70	Sequence 70, Appl
903	21	2.1	437	4	US-09-480-884A-74	Sequence 74, Appl	976	21	2.1	536	4	US-09-123-912-74	Sequence 70, Appl

977 21 2.1 536 4 US-09-643-597-70
978 21 2.1 536 4 US-09-480-884A-70
979 21 2.1 536 4 US-09-542-615A-70
980 21 2.1 536 4 US-09-608-421B-70
981 21 2.1 536 4 US-09-221-107-70
982 21 2.1 540 4 US-09-313-434C-15
983 21 2.1 543 4 US-09-904-615-33
984 21 2.1 548 4 US-09-186-276B-51
985 21 2.1 548 4 US-08-842-445-51
986 21 2.1 548 4 US-09-185-188B-51
987 21 2.1 552 4 US-09-621-976-2737
988 21 2.1 554 4 US-09-696-169A-14
989 21 2.1 557 4 US-09-439-313-384
990 21 2.1 557 4 US-09-352-616A-384
991 21 2.1 557 4 US-09-636-215-384
992 21 2.1 557 4 US-09-685-166A-384
993 21 2.1 565 4 US-09-583-733C-6
994 21 2.1 566 1 US-08-211-942-10
995 21 2.1 568 1 US-08-582-257-20
996 21 2.1 568 2 US-08-582-298-20
997 21 2.1 569 3 US-09-328-111-561
998 21 2.1 570 1 US-07-822-966B-1
999 21 2.1 572 4 US-09-696-169A-12
1000 21 2.1 572 4 US-09-424-978B-32

ALIGNMENTS

RESULT 1
US-08-671-320-15
; Sequence 16, Application US/08671320
; Patent No. 5840558
; GENERAL INFORMATION:
; APPLICANT: VIERLING JR., RICHARD A
; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
; ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 1125 SO. 103RD STREET
; STREET: SUITE 330
; CITY: OMAHA
; STATE: NE
; COUNTRY: US
; ZIP: 68124-1076

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,320
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
TELEFAX: 402-398-9005
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..38
FEATURE:
NAME/KEY: CDS

; LOCATION: 39..977
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 978..1167
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 39..101
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 102..977
; US-08-671-320-16

Query Match 2.7%; Score 27; DB 2; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TTTTGATAAAAAAAAAAAAAAAAAAAAA 982
|||||
Db 1139 TTTTGATAAAAAAAAAAAAAAAAAAAAA 1165
|||||

RESULT 2
US-08-868-577-16
; Sequence 16, Application US/08868577
; Patent No. 586695
; GENERAL INFORMATION:
; APPLICANT: Vierling Jr., Richard A

; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
; ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: 555 13th Street NW, Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,577
FILING DATE: 04-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jondle, Robert J.

REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
TELEFAX: 402-333-1510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..38
FEATURE:
NAME/KEY: CDS
LOCATION: 39..977
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 978..1167
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 39..101
FEATURE:


```

1 TITLE OF INVENTION: NO. 6001639e1 Endoglucanases
2
3 NUMBER OF SEQUENCES: 109
4
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: NO. 6001639o No. 6001639disk of No. 6001639th America, Inc.
7 STREET: 405 Lexington Avenue, 64th Floor
8 CITY: New York
9 STATE: New York
10 COUNTRY: United States of America
11 ZIP: 10174-6401
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC Compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/651,136C
20 FILING DATE: 21-May-1996
21 CLASSIFICATION: 435
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Lambiris, Elias J.
24 REGISTRATION NUMBER: 33,728
25 REFERENCE/DOCKET NUMBER: 4366.200-US
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 212-867-0123
28 TELEFAX: 212-878-9655
29
30 INFORMATION FOR SEQ ID NO: 7:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 1154 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: CDNA
37 FEATURE:
38 NAME/KEY: CDS
39 LOCATION: 51..935
40
41 US-08-651-136C-7
42
43 Query Match 2.6%; Score 26; DB 3; Length 1154;
44 Best Local Similarity 100.0%; Pred.No. 0.022;
45 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
46
47 QY 957 TTGTATAAAAAAAAAAAAAAAAAAAAAA 982
48
49 Db 1091 TTGTATAAAAAAAAAAAAAAAAAAAAAA 1116
50
51 RESULT 5
52 US-09-229-911A-7
53 Sequence 7, Application US/09229911A
54 Patent No. 6387690
55 GENERAL INFORMATION:
56 APPLICANT: Schulein, Martin
57 Lassen, Soren F.
58 Andersen, Lene N.
59 Kauppinen, Markus S.
60 Lange, Lene
61 Nielsen, Ruby I.
62 Ihara, Michiko
63 Takagi, Shinobu
64
65 TITLE OF INVENTION: NO. 6387690e1 Endoglucanases
66
67 NUMBER OF SEQUENCES: 109
68 CORRESPONDENCE ADDRESS:
69 ADDRESSEE: NO. 6387690o No. 6387690disk of No. 6387690th America, Inc.
70 STREET: 405 Lexington Avenue, 64th Floor
71 CITY: New York
72 STATE: New York
73 COUNTRY: United States of America
74 ZIP: 10174-6401
75
76 COMPUTER READABLE FORM:
77 MEDIUM TYPE: Floppy disk
78 COMPUTER: IBM PC Compatible
79 OPERATING SYSTEM: PC-DOS/MS-DOS
80 SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/229,911A
; FILING DATE: 13-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/651,136
; FILING DATE: 21-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4366.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..935
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-229-911A-7

Query Match 2.6%; Score 26; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 957 TTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 1091 TTGATAAAAAAAAAAAAAAAAAAAAA 1116

RESULT 6
5188642-3
; Patent No. 5188642
; APPLICANT: SHAH, DILIP M.; ROGERS, STEPHEN G.; HORSCH, ROBERT B.
; FRALEY, ROBERT T.
; TITLE OF INVENTION: GLYPHOSPHATE-RESISTENT PLANTS
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/478,794
; FILING DATE: 12-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 879,814
; FILING DATE: 7-JUL-1986
; APPLICATION NUMBER: 792,390
; FILING DATE: 29-OCT-1985
; APPLICATION NUMBER: 763,482
; FILING DATE: 07-AUG-1985
; SEQ ID NO: 3:
; LENGTH: 1978
5188642-3

Query Match 2.6%; Score 26; DB 6; Length 1978;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 957 TTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 1939 TTGATAAAAAAAAAAAAAAAAAAAAA 1964

RESULT 7
US-09-640-173-77/c
; Sequence 77, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.

; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-77

Query Match 2.5%; Score 25; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 958 TTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 36 TTGATAAAAAAAAAAAAAAAAAAAAA 12

RESULT 8
US-09-713-550-77/c
; Sequence 77, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-77

Query Match 2.5%; Score 25; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 958 TTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 36 TTGATAAAAAAAAAAAAAAAAAAAAA 12

RESULT 9
US-08-893-654B-5
; Sequence 5, Application US/08893654B
; Patent No. 6165748
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA, ET ALIA
; TITLE OF INVENTION: FRAZZLED NUCLEOTIDE SEQUENCES,
; TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CAMBRIDGE PARK DRIVE
; CITY: CAMBRIDGE
; STATE: MA

; ORGANISM: squalus acanthias
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (439)...(3522)
 US-09-162-021B-1

Query Match 2.5%; Score 25; DB 4; Length 4134;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
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 Db 4075 TTGATATAAAAAAAAAAAAAAAAAAAAA 4099

RESULT 13

US-09-687-477-17
 ; Sequence 17, Application US/09687477
 ; Patent No. 6463883
 ; GENERAL INFORMATION:
 ; APPLICANT: AquaBio Product Sciences, LLC
 ; APPLICANT: Harris, H. William, Jr.
 ; APPLICANT: Russell, David R.
 ; APPLICANT: Nearing, Jacqueline
 ; APPLICANT: Betka, Marlies
 ; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
 ; FILE REFERENCE: 2213.1004-000
 ; CURRENT APPLICATION NUMBER: US/09/687,477
 ; CURRENT FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 4134
 ; TYPE: DNA
 ; ORGANISM: Dogfish Shark
 US-09-687-477-17

Query Match 2.5%; Score 25; DB 4; Length 4134;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
 |||||
 Db 4075 TTGATATAAAAAAAAAAAAAAAAAAAAA 4099

RESULT 14

US-09-687-476-17
 ; Sequence 17, Application US/09687476
 ; Patent No. 6475792
 ; GENERAL INFORMATION:
 ; APPLICANT: AquaBio Product Sciences, LLC
 ; APPLICANT: Harris, H. William, Jr.
 ; APPLICANT: Russell, David R.
 ; APPLICANT: Nearing, Jacqueline
 ; APPLICANT: Betka, Marlies
 ; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
 ; FILE REFERENCE: 2213.2001-000
 ; CURRENT APPLICATION NUMBER: US/09/687,476
 ; CURRENT FILING DATE: 2000-10-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 4134
 ; TYPE: DNA
 ; ORGANISM: Dogfish Shark
 US-09-687-476-17

Query Match 2.5%; Score 25; DB 4; Length 4134;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
 |||||
 Db 4075 TTGATATAAAAAAAAAAAAAAAAAAAAA 4099

RESULT 15

US-09-687-372-17
 ; Sequence 17, Application US/09687372
 ; Patent No. 6481379
 ; GENERAL INFORMATION:
 ; APPLICANT: AquaBio Product Sciences, LLC
 ; APPLICANT: Harris, H. William, Jr.
 ; APPLICANT: Russell, David R.
 ; APPLICANT: Nearing, Jacqueline
 ; APPLICANT: Betka, Marlies
 ; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
 ; FILE REFERENCE: 2213.2002-000
 ; CURRENT APPLICATION NUMBER: US/09/687,372
 ; CURRENT FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 4134
 ; TYPE: DNA
 ; ORGANISM: Dogfish Shark
 US-09-687-372-17

Query Match 2.5%; Score 25; DB 4; Length 4134;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
 |||||
 Db 4075 TTGATATAAAAAAAAAAAAAAAAAAAAA 4099

Search completed: September 26, 2004, 02:47:09
 Job time : 97.9913 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 27, 2004, 09:10:49 ; Search time 92.3848 Seconds
(without alignments)
709.543 Million cell updates/sec

Title: US-10-069-527-4

Perfect score: 1216

Sequence: 1 MARGKIEIKLIENQTNQVY.....RHGGSSIGSSITLHLRLA 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A Genesecp29Jan04:*
- 2: Genesecp1980s:*
- 3: Genesecp1980s:*
- 4: Genesecp2000s:*
- 5: Genesecp2001s:*
- 6: Genesecp2002s:*
- 7: Genesecp2003as:*
- 8: Genesecp2003bs:*
- 9: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1216	100.0	232	4	Aau00187 Granny Sm
2	709.5	58.3	227	4	Aab68435 Amino aci
3	709.5	58.3	227	5	Abg30865 Poplar pr
4	709.5	58.3	227	7	Abu61893 Poplar ho
5	701.5	57.7	227	3	Aay58654 Poplar pt
6	641.5	52.8	231	2	Aar43385 Product O
7	616.5	50.7	227	5	Aae25757 Soybean A
8	595.5	48.1	233	3	Aab32552 Eucalyptu
9	569	46.8	232	3	Aag25577 Arabidops
10	569	46.8	242	3	Aag25576 Arabidops
11	564	46.4	232	3	Aag54029 Arabidops
12	564	46.4	236	3	Aag54679 Arabidops
13	564	46.4	241	3	Aag54028 Arabidops
14	553.5	45.5	227	5	Aae25755 Corn AP3
15	548	45.1	224	5	Aae25763 Rice MAD3
16	488	40.1	171	3	Aag25218 Arabidops
17	488	40.1	181	3	Aag25217 Arabidops
18	419	34.5	108	3	Aab33227 Eucalyptu
19	410.5	33.8	195	3	Aab33164 Eucalyptu
20	364	29.9	186	3	Aag25578 Arabidops
21	359	29.5	186	3	Aag54030 Arabidops
22	355.5	29.2	215	4	Aau00186 Granny Sm
23	331.5	27.3	208	3	Aag21899 Arabidops
24	326	26.8	210	2	Aar46555 fbpl, for
25	313.5	25.8	209	5	Abg60942 Novel flo

26	312.5	25.7	209	5	ABG60945	Novel flo
27	311.5	25.6	260	5	ABG60932	Novel flo
28	310.5	25.5	209	5	ABG60941	Novel flo
29	308.5	25.4	209	5	AAE25756	Corn AP3
30	305.5	25.1	240	4	AAE25756	Maize ZmM
31	305.5	25.1	240	4	AAE25756	Maize ZmM
32	305.5	25.1	240	4	AAE25756	Maize ZmM
33	298	24.5	212	3	AAE26345	Corn nitr
34	296.5	24.4	221	3	AAE26345	Zea mays
35	296	24.3	241	2	AAE26345	Arabidops
36	295	24.3	249	2	AAE26345	Arabidops
37	294.5	24.2	249	3	AAE26345	Rice OSM
38	293.5	24.1	260	5	AAE26345	Arabidops
39	291	23.9	244	3	AAE26345	Novel flo
40	290.5	23.9	238	5	AAE26345	Novel flo
41	290.5	23.9	238	5	AAE26345	Novel flo
42	290.5	23.9	238	5	AAE26345	Novel flo
43	290	23.8	210	6	AAE26345	Arabidops
44	289	23.8	205	5	AAE26345	Arabidops
45	288.5	23.7	228	3	AAE26345	Arabidops

ALIGNMENTS

RESULT 1

AAU00187

ID AAU00187 standard; peptide; 232 AA.

XX AAU00187;

XX AAU00187;

DT 11-SEP-2003 (revised)

DT 17-MAY-2001 (first entry)

XX AAU00187;

XX AAU00187;

XX AAU00187;

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XX AAU00187;

XX AAU00187;

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XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

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XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
 CC for use in an accelerated breeding programme to produce seedless fruit.
 CC They may also be used in designing probes and primers for MdPI or MdAP3,
 CC or their variants. The seedless fruiting plant is more convenient than
 CC seeded fruit since these can be cropped without pollination, reducing
 CC dependence on bees, pollinator varieties and warm weather at flowering.
 CC The absence of pollen is also advantageous to alleviate environmental
 CC concerns regarding the transfer of transgenes to non-transgenic by cross
 CC pollination. Seedless cultivars can also avoid or reduce biennial bearing
 CC tendencies that have been attributed to the inhibition of flower bud
 CC formation by developing seeds and are less susceptible to codling moth
 CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX SQ Sequence 232 AA;

Query Match 100.0%; Score 1216; DB 4; Length 232;
 Best Local Similarity 100.0%; Pred. No. 1.1e-105; Indels 0; Gaps 0;
 Matches 232; Conservative 0; Mismatches 0;
 QY 1 MARGKIEIKLIENQTNQVTSKRRNGIFPKAQELTVLCAKVSILMLNTNKKHVEYISP 60
 DB 1 MARGKIEIKLIENQTNQVTSKRRNGIFPKAQELTVLCAKVSILMLNTNKKHVEYISP 60
 QY 61 TTTTSMYDDYQKTGIDLWRTHESSMKDTLWKLKEINNKLRREIRORLGHDLNGLSFDE 120
 DB 61 TTTTSMYDDYQKTGIDLWRTHESSMKDTLWKLKEINNKLRREIRORLGHDLNGLSFDE 120
 QY 121 LASLDEMOSSLDAIRQKHYVTKQTETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 DB 121 LASLDEMOSSLDAIRQKHYVTKQTETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 QY 181 GYEDNEGDYESALNSGANNLYTFHLHH-----PNLHGGSSIGSSITLHDLRLA 232
 DB 181 GYEDNEGDYESALNSGANNLYTFHLHH-----PNLHGGSSIGSSITLHDLRLA 232

RESULT 2
 AAB68435
 ID AAB68435 standard; protein; 227 AA.
 XX AAB68435;
 AC
 XX 23-JUL-2001 (first entry)
 DT
 XX Amino acid sequence of the floral homeotic protein PTD.
 DE
 XX
 KW Floral homeotic gene; PDF; PRLP; PTAG-1; PTAG-2; floral tissue; LEAFY;
 KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KW fertility; sterility.
 XX
 OS Populus balsamifera.

XX Key Location/Qualifiers
 XX Domain 1..57
 FT /note= "MADS domain"
 FT Domain 87..154
 FT /note= "K-domain"
 XX CA2319853-A1.
 XX 01-APR-2001.
 XX 02-OCT-2000; 2000CA-02319853.
 XX 01-OCT-1999; 99US-00410464.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 XX Rottman WH, Strauss SH, Brunner AM, Sheppard LA;
 XX WPI; 2001-336098/36.
 XX N-PSDB; AAF85391, AAF85392, AAF85393.

XX Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,
 PT particularly sterility.
 PS Claim 23; Page 43-44; 69pp; English.
 XX The present sequence represents a floral homeotic protein, designated
 CC PDF. It is derived from Populus balsamifera subsp. trichocarpa. The
 CC specification also describes PRLP, PTAG-1 and PTAG-2 proteins. The floral
 CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of
 CC LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility
 XX SQ Sequence 227 AA;

Query Match 58.3%; Score 709.5; DB 4; Length 227;
 Best Local Similarity 62.3%; Pred. No. 3.6e-58;
 Matches 149; Conservative 24; Mismatches 45; Indels 21; Gaps 5;
 QY 1 MARGKIEIKLIENQTNQVTSKRRNGIFPKAQELTVLCAKVSILMLNTNKKHVEYISP 60
 DB 1 MARGKIEIKLIENQTNQVTSKRRNGIFPKAQELTVLCAKVSILMLNTNKKHVEYISP 60
 QY 61 TTTTSMYDDYQKTGIDLWRTHESSMKDTLWKLKEINNKLRREIRORLGHDLNGLSFDE 120
 DB 61 STSTKTIYDQKNALGIDLWGTQYKQEHRLKLNLDINHLRQEIQRGEGLDLSIDH 120
 QY 121 LASLDEMOSSLDAIRQKHYVTKQTETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 DB 121 LRGLQEHTEALNGVRGRKHVTKQNETYRKVKYKLEERHGNLMLEY---EAKLEDQY 177
 QY 181 GYEDNEGDYESALNSGANNLYTFHLHH-----PNLHGGSSIGSSITLHDLRL 231
 DB 178 GLVDN----EAAVALANGASNLVAFRLHGHGHHHHLPNLHL-GDGFGA-----HEURL 226

RESULT 3
 ABG30865
 ID ABG30865 standard; protein; 227 AA.
 XX ABG30865;
 AC
 XX 29-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX Poplar protein transduction domain, PTD, protein.
 XX Poplar; plant; DEFICIENS; transgenic; promoter;
 KW protein transduction domain; floral homeotic gene;
 KW floral-specific expression; cytotoxin; fertility; sterility; PTLF;
 KW PTAG-1; PTAG-2.
 XX Populus balsamifera; subsp. trichocarpa.
 XX Key Location/Qualifiers
 XX Domain 1..57
 FT /label= "MADS domain"
 FT /note= "MADS" is named for the first 4 proteins in which
 FT it was discovered, yeast minichromosome maintenance
 FT factor, floral homeotic genes AG and DEF and human serum
 FT response factor"
 FT 87..154
 FT /label= "K-domain"
 XX US6395892-B1.
 XX 28-MAY-2002.

XX 01-OCT-1999; 99US-00410464.
XX 06-APR-1998; 98US-0080851P.
PR 06-APR-1999; 99US-00287700.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX WPI; 2002-572853/61.
DR N-PSDB; ABK88484, ABK88485.
XX New protein transduction domain promoter nucleic acid molecule useful for
PT producing transgenic plants having modified fertility characteristics,
PT particularly sterility.
XX Disclosure; Col 39-42; 46pp; English.
XX The invention relates to an isolated nucleic acid molecule especially a
CC protein transduction domain (PTD) promoter; (i) that hybridises under
CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 x SDS (sodium
CC dodecyl sulphate) at 65 plusOC to nucleotides or (ii) comprising 35
CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
CC and is the homologue of DEFICIENS. Also includes are a recombinant
CC nucleic acid comprising the PTD promoter, a cell transforming with the
CC recombinant nucleic acid and a transgenic plant comprising the
CC transduced cell. The PTD promoter is useful to obtain floral-specific
CC expression of genes such as cytotoxins, that are employed in genetic
CC ablation strategies to produce trees having modified fertility
CC characteristics, including sterility. Genetic constructs comprising
CC antisense versions or dominant negative mutants of PTD are useful in
CC producing genetically engineered Poplars and other trees, and for sense
CC suppression. Also disclosed are 3 other homeotic genes PTF, PTAG-1 and
CC PTAG-2 (none are defined). The present sequence is the PTD protein.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 227 AA;
Query Match 58.3%; Score 709.5; DB 5; Length 227;
Best Local Similarity 62.3%; Pred. No. 3.6e-58;
Matches 149; Conservative 24; Mismatches 45; Indels 21; Gaps 5;
QY 1 MARGKIEIKLIENQTRQVTSKRNGIFPKAQELTVLCAKSLMLNTNKHVEYISP 60
DB 1 MGRGKIEIKKIENPTNRQVTSKRNGIFPKAQELTVLCAKSLMLNFSNTNKLNEYISP 60
QY 61 TTTTSMYDDYQKTMGIDLRWTHESKMDTLWLKKEINNKLRREIRQRGLHDLNGLSFDE 120
DB 61 STSTKKIYDQYQNALGIDLMGTQYKMQEHLRKLNDINHKLQRIQRQRGEGDLSIDH 120
QY 121 LASLDDMQSSLDAIRQRKYHVIKTQTETTKKKVKNLEQRGNMLHGYFDQEAAGDPQY 180
DB 121 LRGLQHMTEALNGVRGRKYHVIKTQNETYRKVKKNLEERGNLMLEY---EAKLEDQY 177
QY 181 GYEDNEGDEYASALNSGANNLYTFHLH-----PNLHGGSSLSGSSITHLHLRL 231
DB 178 GLVDN-----EAAVALANGASNDYAPRLHGHGHHHLPNHLH-GDGFGA-----HELR 226
RESULT 4
ID ABU61893
XX ABU61893 standard; protein; 227 AA.
XX AC ABU61893;
XX 18-AUG-2003 (first entry)
XX Poplar homeotic protein PTD.
XX Poplar; PTD; deficiencies; homeotic gene; floral development; sterile tree;
KW pulp; paper; plant.
XX

OS Populus balsamifera subsp. trichocarpa.
XX Key Location/Qualifiers
FH 1..57
FT Domain /label= MADS_domain
FT Domain 87..154
FT /label= K_domain
XX US2003033628-A1.
XX 13-FEB-2003.
XX 21-MAR-2002; 2002US-00104580.
XX 06-APR-1998; 98US-0080851P.
PR 06-APR-1999; 99US-00287700.
PR 01-OCT-1999; 99US-00410464.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX WPI; 2003-466273/44.
DR N-PSDB; ACA62517, ACA62518.
XX New floral homeotic nucleic acid molecules, useful for the manipulation
PT of flowering in Poplar and other plant species, and for producing
PT transgenic plants having modified fertility characteristics, particularly
PT sterility.
XX Claim 23; Page 22; 48pp; English.
XX The invention relates to an isolated nucleic acid molecule comprising at
CC least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
CC 4 homeotic genes from poplar, PTF (LEAFY and FLORICA homologue), PTD
CC (DEFICIENS homologue), and PTAG-1/PTAG-2 (both homologues of AGAMOUS).
CC Also included are a recombinant nucleic acid molecule comprising a
CC promoter sequence operably linked to the nucleic acid molecule, a cell
CC transformed with the nucleic acid molecule, a transgenic plant comprising
CC the recombinant nucleic acid molecule and the purified proteins encoded
CC by the nucleic acids. The nucleic acid molecules are useful for the
CC manipulation of flowering in Poplar and other plant species, for
CC producing transgenic plants having modified fertility characteristics
CC (particularly sterility) and in the pulp and paper industries. The
CC present sequence is the poplar PTD protein
XX
SQ Sequence 227 AA;
Query Match 58.3%; Score 709.5; DB 7; Length 227;
Best Local Similarity 62.3%; Pred. No. 3.6e-58;
Matches 149; Conservative 24; Mismatches 45; Indels 21; Gaps 5;
QY 1 MARGKIEIKLIENQTRQVTSKRNGIFPKAQELTVLCAKSLMLNTNKHVEYISP 60
DB 1 MGRGKIEIKKIENPTNRQVTSKRNGIFPKAQELTVLCAKSLMLNFSNTNKLNEYISP 60
QY 61 TTTTSMYDDYQKTMGIDLRWTHESKMDTLWLKKEINNKLRREIRQRGLHDLNGLSFDE 120
DB 61 STSTKKIYDQYQNALGIDLMGTQYKMQEHLRKLNDINHKLQRIQRQRGEGDLSIDH 120
QY 121 LASLDDMQSSLDAIRQRKYHVIKTQTETTKKKVKNLEQRGNMLHGYFDQEAAGDPQY 180
DB 121 LRGLQHMTEALNGVRGRKYHVIKTQNETYRKVKKNLEERGNLMLEY---EAKLEDQY 177
QY 181 GYEDNEGDEYASALNSGANNLYTFHLH-----PNLHGGSSLSGSSITHLHLRL 231
DB 178 GLVDN-----EAAVALANGASNDYAPRLHGHGHHHLPNHLH-GDGFGA-----HELR 226
RESULT 5
ID AAY58654
XX AAY58654 standard; protein; 227 AA.
XX

AC AAY58654;
 XX 11-APR-2000 (first entry)
 XX Poplar PTD floral homeotic gene-encoded protein.
 DE Poplar; PTD; floral homeotic gene; transgenic plant; sterility;
 KW fertility.
 XX Populus balsamifera subsp. trichocarpa.
 OS
 XX Key Location/Qualifiers
 FH Domain 1..60
 FT /note= "MADS domain"
 FT Domain 88..143
 FT /note= "K domain"
 XX CA2227940-Al.
 PN
 XX 06-OCT-1999.
 PD
 XX 07-APR-1998; 98CA-0227940.
 PF
 XX 06-APR-1998; 98US-00080851.
 PR
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
 PI WPI, 2000-106662/10.
 XX N-PSDB; AAZ57942, AAZ57943.
 DR
 XX Nucleic acid from Populus trichocarpa genes, useful for producing
 PT transgenic plants, particularly trees, with modified fertility
 PT characteristics such as sterility.
 XX
 PS Claim 31; Page 49-50; 92pp; English.

XX The present sequence is that of the novel PTD protein of poplar (Populus
 CC balsamifera subsp. trichocarpa), as deduced from newly isolated PTD gene
 CC and cDNA sequences (see AAZ57942-43). PTD is 1 of 4 novel floral homeotic
 CC genes identified in this poplar species. It is a homologue of DEFICIENS
 CC and is expressed strongly in stamen primordia from the onset of
 CC organogenesis, and is also expressed at low levels in carpel primordia.
 CC PTD contains both a MADS domain and a K-domain. The invention provides
 CC nucleic acid sequences of the 4 novel Populus genes, the corresponding
 CC cDNA sequences (see AAZ47942-49) and deduced amino acid sequences (see
 CC AAY58454-57). It also provides methods of using the gene and cDNA
 CC sequences to produce genetically engineered Populus and other trees
 CC having modified fertility characteristics, including sterility. Genetic
 CC constructs useful in producing genetically engineered Populus and other
 CC trees include antisense versions of PTD, dominant negative mutants, and
 CC constructs useful for sense suppression. Sterile trees allow increased
 CC wood yield and a reduction in the production of allergens such as pollen
 CC
 XX Sequence 227 AA;

Query Match 57.7%; Score 701.5; DB 3; Length 227;
 Best Local Similarity 61.5%; Pred. No. 28-57;
 Matches 147; Conservative 26; Mismatches 45; Indels 21; Gaps 5;
 QY 1 MARGKIEIKLIENQTNQVTSYKRRNGIFPKAQLTCLCDKAVSLIMLNTNKGHEVISP 60
 DB 1 MGRKIEIKLIENPTNQVTSYKRRNGIFPKAQLTCLCDKAVSLIIVPTNKLEVISP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHESKMDTLWKLKEINNKLRREIRORLGHDLNGLSFDE 120
 DB 61 STTKTYDQYQNALGIDLWGTQYKMQEHLKRLNDINHKLROEIRQRGEGNDLSIDH 120
 QY 121 LASIDDEMOSLDAIRQKXHVIKTQTTETTKKVKVLEQRGNMLHGYFDQAAGEDPOY 180
 DB 121 LRGLEQHWTEALNGVRGKXHVIKTQNETYRKVKVLEERHGNLNEY---EAKLEDROY 177

QY 181 GYEDNEGDYESALALNSGANNLYTFHLH-----PNLHHGSSSLGSSITHLHDLRL 231
 DB 178 GLVDN-----EAAVALANGASNDYAPRLHHGHNNHHHLPNLHL-GDGFGA-----HELRL 226

RESULT 6
 AAR43385
 ID AAR43385 standard; protein; 231 AA.
 XX AAR43385;
 XX 25-MAR-2003 (revised)
 DT 19-JUN-1994 (first entry)
 XX Product of homeotic gene green petal.
 DE Plant; organ morphogenesis; control; petunia; petals.
 XX Petunia.
 XX WO9321322-Al.
 PN 28-OCT-1993.
 PD 13-APR-1993; 93WO-US003508.
 PF 13-APR-1992; 92US-00867580.
 PR 06-JUL-1992; 92US-00909589.
 XX (UYRQ) UNIV ROCKEFELLER.
 PA Halfter U, Van Der Krol AR, Kush A, Chua N;
 PI WPI, 1993-351732/44.
 DR N-PSDB; AAQ51169.
 XX Plant organ morphogenesis control and determ. - by regulating the
 PT expression of homeotic genes which determine the identity of the organ.

XX Disclosure; Fig 2; 74pp; English.
 XX The homeotic gene green petal from petunia has been cloned and
 CC characterised previously. The gene was used in a new method for
 CC controlling the morphogenesis of plant organs comprising regulating the
 CC expression of the gene using ectopic expression. Such a method can be
 CC used to determine and control plant organ morphogenesis, such as
 CC modifying petals without altering the reproductive portions of the
 CC flower. See also AAR43386-7. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX Sequence 231 AA;

Query Match 52.8%; Score 641.5; DB 2; Length 231;
 Best Local Similarity 55.6%; Pred. No. 8.7e-52;
 Matches 129; Conservative 36; Mismatches 52; Indels 15; Gaps 4;
 QY 1 MARGKIEIKLIENQTNQVTSYKRRNGIFPKAQLTCLCDKAVSLIMLNTNKGHEVISP 60
 DB 1 MARGKIQIKRIENQTNQVTSYKRRNGIFPKANETLVLCDAKVSIIISSTGKLHEFISP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHESKMDTLWKLKEINNKLRREIRORLGHDLNGLSFDE 120
 DB 61 SITTKQLFDLYQKTVGVLDLWNSHYEKMQEQLKLEKVNRLKEIRORMGESLNDLNEYQ 120
 QY 121 LASIDDEMOSLDAIRQKXHVIKTQTTETTKKVKVLEQRGNMLHGYFDQAAGEDPOY 180
 DB 121 LEELMENVDNSLKLIREKXVIGNQIETPKKVRNVEIHRNLL---LEFDARQEDP-Y 176
 QY 181 GYEDNEGDYESALALNSGANNLYTFHL-----HFNLHHGSSSLGSSIT 224
 DB 177 GLVQEGDYSVLGFPNGGHRILALRQPNHQPNNHHHLLHSG---GSDIT 225

RESULT 7
AAE25757
ID AAE25757 standard; protein; 227 AA.
XX
AC
AC AAE25757;
XX
DT 04-NOV-2002 (first entry)
XX
DE Soybean AP3 homologue protein from clone sflin.pk001.116.
XX
KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
KW sterility; plant growth; inflorescence architecture; plant morphology;
KW tissue culture; cell division; soybean.
XX
OS Glycine max.
XX
FN W0200244390-A2.
XX
PD 06-JUN-2002.
XX
PF 21-NOV-2001; 2001WO-US043750.
XX
PR 28-NOV-2000; 2000US-0253415P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon EB, Cahoon RE, Klein TW, Rafalski AJ, Sakai H;
XX
DR WPI; 2002-547703/58.
XX
DR N-PSDB; AAD42259.
XX

XX New floral developmental polypeptide having flowering locus T or Ap3
PT homolog activity, useful for immunological screening of cDNA expression
PT libraries.
XX
PS Claim 17; Page 80-81; 88pp; English.
XX
CC The present invention relates to novel floral developmental proteins,
CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
CC proteins and polynucleotides encoding such proteins. Floral developmental
CC polynucleotides are useful for transforming cells or for producing plants
CC by transforming the plant cells with the polynucleotides and regenerating
CC the plants from the transformed plant cells. Sequences of the invention
CC are useful for immunological screening of cDNA expression libraries. They
CC are also useful for creating transgenic plants. Polynucleotides of the
CC invention are used as probes for genetically and physically mapping the
CC genes that they are a part of and as markers for traits linked to those
CC genes. AP3 homologues may be useful for engineering plant sterility or
CC fertility, flower development and morphology. FT or FT11 homologues are
CC useful for engineering flowering time, plant growth rate, inflorescence
CC architecture, tissue culture morphology and rate of cell division to
CC enhance transformation. The present sequence is soybean AP3 homologue
CC protein
XX
SQ Sequence 227 AA;

Query Match 50.7%; Score 616.5; DB 5; Length 227;
Best Local Similarity 52.2%; Pred. NO. 1.9e-49;
Matches 118; Conservative 41; Mismatches 60; Indels 7; Gaps 3;

QY 1 MARGKTEIKLIENTNQNTQVTSKRRNGIFPKKAQELTVLCDKAVSLIMLNTNKHHEYISIP 60
DB 1 MARGKTIQKLIENNTNRQVTSKRRNGIFPKKANLTVLCDKAVSLIMFSSTGKLHGYISIP 60
QY 61 TTTTSGMYDDYQKTMGIDLWRTHESMDTLWKLEINNKLRREIRORLGHDLNGLSPDE 120
DB 61 STSTKQFFDQYQMTLGVDLWNSHYENQENLKKLEVNRLAKEIRRMGDCNLGLNED 120
QY 121 LASLDDMQSSLDALRQKRYHVIKTQETTTKKKYNLEORRNMLHGVFDQEAAGEDPQY 180
DB 121 LKLEBEMDAKAAKVRERKVIITNQIDTQKKNFNEKEVNRLLH---DLDAKAEPRF 177

QY 181 GYEDNEGDYESALALNSGANNLYTFHLH--HPNHLHGSSSLGSSIT 224
DB 178 ALIDNGGEVESVIGFNLGFRMFALSIOQSPHPSAHSGGA--GSDLT 221

RESULT 8

AAE25757
ID AAE25757 standard; protein; 233 AA.
XX
AC AAE25757;
XX
DT 25-JAN-2001 (first entry)
XX
DE Eucalyptus grandis transcription factor: protein sequence #10.

XX
KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB.
XX
OS Eucalyptus grandis.
XX
FN W0200053724-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006112.
XX
PR 11-MAR-1999; 99US-00266513.
PR 18-AUG-1999; 99US-0149485P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Wood M, Mcgrath A, Shenk MA, Glenn M;
XX
DR WPI; 2000-579369/54.

XX New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide.
XX
PS Claim 8; Page 203; 747pp; English.
XX
CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
CC transcription factor. The transcription factor may be used to produce a
CC plant having modified gene expression such as a woody plant e.g. a
CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
CC to modify the activity of a polypeptide in a plant. The transcription
CC factors of the present invention are members from the following families
CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2
CC Cys2His2, CCAAT box elements and MYB
XX
SQ Sequence 233 AA;

Query Match 48.1%; Score 585.5; DB 3; Length 233;
Best Local Similarity 51.3%; Pred. No. 1.6e-46;
Matches 118; Conservative 40; Mismatches 63; Indels 9; Gaps 4;

QY 1 MARGKTEIKLIENTNQNTQVTSKRRNGIFPKKAQELTVLCDKAVSLIMLNTNKHHEYISIP 60
DB 1 MARGKTIQKLIENNTNRQVTSKRRNGIFPKKANLTVLGDPKVSIIMTSSTGKLHGYISIP 60
QY 61 TTTTSGMYDDYQKTMGIDLWRTHESMDTLWKLEINNKLRREIRORLGHDLNGLSPDE 120
DB 61 STSTKQFFDQYQMTLGVDLWNSHYENQENLKKLEVNRLAKEIRRMGDCNLGLNED 120
QY 121 LASLDDMQSSLDALRQKRYHVIKTQETTTKKKYNLEORRNMLHGVFD--QEAAGEDP 178

Db	121	LCGLQMDMNAVSLIRKKYKTLGNQIDTARKKKKNAEINKSLLODWTNLIKHLREDDP	180
Qy	179	QYGYEDNEGDIYESALALSN--GANNLYTFHLH--HFNLAHGSSLSGSIT	224
		: : : : : :	
Db	181	HFGVMDNGRDYEAVIGVTDAAARLYTLRLQPDQNLITSGG--GSEIT	227
		: : : : : :	
RESULT 9			
AAG25577	ID	AAG25577 standard; protein; 232 AA.	
XX	AC	AAG25577;	
XX	DT	17-OCT-2000 (first entry)	
DE	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 29698.	
XX	XX		
KW	KW	Protein identification; signal transduction pathway; metabolic pathway;	
KN	KN	hybridisation assay; Genetic mapping; gene expression control; promoter;	
XX	XX	termination sequence.	
OS	OS	Arabidopsis thaliana.	
PN	PN	EP1033405-A2.	
XX	XX	06-SEP-2000.	
PD	PD		
PF	PF	25-FEB-2000; 2000EP-00301439.	
XX	XX		
XX	XX	25-FEB-1999; 99US-0121825P.	
PR	PR	05-MAR-1999; 99US-0123180P.	
PR	PR	09-MAR-1999; 99US-0123548P.	
PR	PR	23-MAR-1999; 99US-0125788P.	
PR	PR	25-MAR-1999; 99US-0126284P.	
PR	PR	29-MAR-1999; 99US-0126785P.	
PR	PR	01-APR-1999; 99US-0127462P.	
PR	PR	06-APR-1999; 99US-0128234P.	
PR	PR	08-APR-1999; 99US-0128714P.	
PR	PR	16-APR-1999; 99US-0129845P.	
PR	PR	19-APR-1999; 99US-0130077P.	
PR	PR	21-APR-1999; 99US-0130449P.	
PR	PR	23-APR-1999; 99US-0130510P.	
PR	PR	23-APR-1999; 99US-0130891P.	
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Query Match	46.8%	Score 569	DB 3	Length 222
Beet Local Similarity	53.3%	Pred. No. 5.5e-45		
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PR 29-OCT-1999; 99US-0162142P.

Query Match 46.8%; Score 569; DB 3; Length 242;
Best Local Similarity 53.3%; Pred. No. 5; 9e-45;
Matches 114; Conservative 30; Mismatches 66; Indels 4; Gaps 2;

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Db 71 NTTTTKEIVDYXQISVDYWAQTOEKGMBETKRLLETRNRLRTQYKQJLGCCLNKLDIOE 130
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Db 131 LRRLEDEMENTFKLVEREKSKPSIGNQIETTKKKKNSQODIQNLITH--EELRAEDBPY 187
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RESULT 11

ID AAG54029 standard; protein; 232 AA.

AC AAG54029;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68844.

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

06-SEP-2000
PD

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PR	01-JUN-1999	99US-01372822P
PR	01-JUN-1999	99US-0137528P
PR	04-JUN-1999	99US-0137502P
PR	04-JUN-1999	99US-0137724P
PR	08-JUN-1999	99US-0138094P
PR	10-JUN-1999	99US-0138540P
PR	10-JUN-1999	99US-0138847P
PR	18-JUN-1999	99US-0139456P
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PR	18-JUN-1999	99US-0139457P
PR	18-JUN-1999	99US-0139458P
PR	18-JUN-1999	99US-0139459P
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PR	18-JUN-1999	99US-0139461P
PR	18-JUN-1999	99US-0139462P
PR	18-JUN-1999	99US-0139463P
PR	18-JUN-1999	99US-0139750P
PR	18-JUN-1999	99US-0139763P
PR	18-JUN-1999	99US-0140091P
PR	30-JUN-1999	99US-0141887P
PR	01-JUL-1999	99US-0141842P
PR	01-JUL-1999	99US-0142154P
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PR	02-AUG-1999	99US-0146386P
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PR	04-AUG-1999	99US-0147204P

Query Match	46.4%;	Score 564;	Da 3;	Length 232;
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DB	1	MARGKIKIKRIENOTNQVYTSKRRNGLFFKAKHETVLCDPARVSIIMFSSSNKILHEIYSP	60
QY	61	TTTTKSNVDDYQKTMGDIWRTHESKMDTLMLKEINNTLRREIRORLGHIDNGLSFDE	120
DB	61	NTTKEIVDLVQYTISSDVDAVATQYERKQETKSKLLETNRNLRFQIKORLGECLDELIDQ	120
QY	121	LASIDDEMOSSLDIRQKRYHVIKTQETTKKKVKNLEQRGNMLHGYFDQEAAGEDPOY	180
DB	121	LRRLEDEMENTFKLYRERKFKESLGNQIETTKKKKSSQODIQKULIH---ELELRADPHY	177
QY	181	GYEDNEGDEVSALASNGANNITFHLHHPNLH	214
DB	178	GLVNDGSDYDSVLGYQTEGSRAYALRPHQ-NHHH	210

RESULT 12	
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ID	AA654679 standard; protein; 236 AA.
AC	AA654679;
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DT	18-OCT-2000 (first entry)
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 69759.
XX	
KM	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
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Query Match 46.4%; Score 564; DB 3; Length 236;
Best Local Similarity 52.8%; Pred. No. 1,7e+44;
Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGKIKIKLENTNQVYTKRRNGIFPKACQELVLCDAKYSILNLTNTNCHYIEP 60
DB 5 MARGKIKIKLENTNQVYTKRRNGIFPKACQELVLCDAKYSILNLTNTNCHYIEP 64
QY 61 TTTTKSVDDYQKMGIDLWRTHEESKMDLWKLKKEINNKLRERIQRLGHDLNGLSFDE 120
DB 65 NTTYKEIVDYQITISPDVWATQYERMOETKRLLETNRIQRIQRLCECLDXID 124
QY 121 LASLIDMOSSLDAIRPKYHVIKTQETTKKKYKNLEGRGMHLGYPQEAAGDEDPY 180
DB 125 LRRLEDEMENTFKLVRRKFKSLGNQLETTKKKKKSOODIQKNLH--ELELRADPHY 181
QY 181 GYEDNEGDEYSAALNSGANNLYTFHLHPNLMH 214
DB 182 GLVDNGGDYDSVLGYQIEGSRAYALRPHQ-NHHH 214

RESULT 13

AA054028 standard; protein; 241 AA.

AA054028;

18-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 68843.

KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

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PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
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PR 25-MAR-1999; 99US-0126264P.
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 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.

PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 25-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 46.4%; Score 564; DB 3; Length 241;
 Best Local Similarity 52.8%; Pred. No. 1,7e-44;
 Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGKIEIKLEIENQTRQYTSKRRNGIFPKAQELTVLCDAKVSLIMLSNTNMHEVISP 60
 DB 10 MARGKIQIKRIENQTRQYTSKRRNGIFPKQHETVLCDAVSTIMSSSKHETVISP 69
 QY 61 TTTTSMYDDYQKTMGIDIMRTHEBSKDTLMKLEINNKLRREIRORIGHDINGLSFDE 120
 DB 70 NNTTKEIVDLVQGISDVVWATQYERMQETKRLLETNNRLTQIKORIGECIDEDHIOE 129
 QY 121 LASLDDEMSSLDATFORKHYIKQOTETKXKKVKNLEGRBNMLGYDQBAAGDPQY 180
 DB 130 LRRLEDEMENTFTXVLERKPKSLGNQIFTKKKNSQDIOQKVLH--ELRLRADPXY 186
 QY 181 GYEDNEGYESALALNSGANNLYTFLLHHPNLH 214
 DB 187 GLVDNGGDYDVLGVIGESRAVALRFQ-NHHH 219

RESULT 14
 AAE25755
 ID AAE25755 standard; protein; 227 AA.
 XX
 AC AAE25755;
 XX
 DT 04-NOV-2002 (first entry)
 XX
 DE Corn AP3 homologue protein from clone ctain.pk0050.f8.
 XX
 KW Floral developmental protein; flowering locus T; APEYAL3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW fertility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; corn.
 XX
 OS Zea mays.
 XX
 PN W0200244390-A2.
 XX
 PD 06-JUN-2002.
 XX
 PE 21-NOV-2001; 2001WO-US043750.
 XX
 PR 28-NOV-2000; 2000US-0253415P.
 XX
 PA (DUPO) DU POINT DE NEMOURS & CO E I.
 XX
 FT Cahoon EB, Cahoon RE, Klein TW, Rafaleki AJ, Sakai H;
 XX
 DR WPI; 2002-547703/58.
 DR N-PSDB; AAD42257.
 XX
 PT New floral developmental polypeptide having flowering locus T or AP3
 PT homology activity; useful for immunological screening of cDNA expression
 FT libraries.
 XX
 PS Claim 18; Page 78; 88pp; English.
 XX
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APEYAL3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental

CC polynucleotides are useful for transforming cells or for producing plants
CC by transforming the plant cells with the polynucleotides and regenerating
CC the plants from the transformed plant cells. Sequences of the invention
CC are useful for immunological screening of cDNA expression libraries. They
CC are also useful for creating transgenic plants. Polynucleotides of the
CC invention are used as probes for genetically and physically mapping the
CC genes that they are a part of and as markers for traits linked to those
CC genes. AP3 homologues may be useful for engineering plant sterility or
CC fertility, flower development and morphology. FT or FTL homologues are
CC useful for engineering flowering time, plant growth rate, inflorescence
CC architecture, tissue culture morphology and rate of cell division to
CC enhance transformation. The present sequence is corn AP3 homologue
CC protein

XX SQ Sequence 227 AA;

Query Match 45.5%; Score 553.5; DB 5; Length 227;
Best Local Similarity 51.0%; Pred. No. 1.5e-43;
Matches 122; Conservative 33; Mismatches 63; Indels 21; Gaps 7;

Qy 1 MARGKIEIKLIENQTRQVYTKRRNGIFPKAQLTVLCDAKVSLMTNTKMGHEYISP 60
Db 1 MGRKIEIKRIENATNRQVYTKRRNGIMKKARELVLCDAQVALIFSSSTGKXHEFCSP 60

Qy 61 TTTTSMVDDYQKTMGIDLWRTHEESKDTLMKKEINNKLRREIRORLGHDLNGLSFDE 120
Db 61 GTDIKTFDREYQQAIGTSLWIEQYENMQRTLSHLKQINRGIRFIRQRMGEDLDGDFDE 120

Qy 121 LASIDDEMOSLDAIRORXHVITKTQETTTKKVKNLEQRGMMLHGFDQBAAG--EPP 178
Db 121 LRGLQNVDAALKEVRHRKXHVISTQIDYKKKXKSHKSHKYNKL-----QDELGRREPP 174

Qy 179 QYGYEDNEG--DYESALALNSGA--NNLYTFHL--HHPNLHGGSSLSGSSITLHDLRL 231
Db 175 AFGVNTGTGAGVAMDGAALGAPDPAFAFRVPSQPNLH--GMAVGG-----FHDRL 226

RESULT 15

AAE25763 ID AAE25763 standard; protein; 224 AA.

XX AAE25763;

XX 04-NOV-2002 (first entry)

XX Rice MADS box-like protein.

XX Floral developmental protein; flowering locus T; APETALA3; transgenic;

KM FT; AP3; transgenic plant; fertility; flower development; gene mapping;

KM sterility; plant growth; inflorescence architecture; plant morphology;

XX tissue culture; cell division; rice; MADS box-like protein.

XX Oryza sativa.

XX MO200244390-A2.

XX 06-JUN-2002.

XX 21-NOV-2001; 2001MO-US043750.

XX 28-NOV-2000; 2000US-0253415P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

XX WPI; 2002-547703/58.

XX New floral developmental polypeptide having flowering locus T or AP3
PT homolog activity, useful for immunological screening of cDNA expression
PT libraries.

XX Example 4; Page 82-83; 88pp; English.

XX The present invention relates to novel floral developmental proteins,
CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
CC proteins and polynucleotides encoding such proteins. Floral developmental
CC polynucleotides are useful for transforming cells or for producing plants
CC by transforming the plant cells with the polynucleotides and regenerating
CC the plants from the transformed plant cells. Sequences of the invention
CC are useful for immunological screening of cDNA expression libraries. They
CC are also useful for creating transgenic plants. Polynucleotides of the
CC invention are used as probes for genetically and physically mapping the
CC genes that they are a part of and as markers for traits linked to those
CC genes. AP3 homologues may be useful for engineering plant sterility or
CC fertility, flower development and morphology. FT or FTL homologues are
CC useful for engineering flowering time, plant growth rate, inflorescence
CC architecture, tissue culture morphology and rate of cell division to
CC enhance transformation. The present sequence is rice MADS box-like
CC protein. This sequence is used in the exemplification of the invention
CC protein

XX SQ Sequence 224 AA;

Query Match 45.1%; Score 548; DB 5; Length 224;
Best Local Similarity 50.2%; Pred. No. 4.9e-43;
Matches 120; Conservative 31; Mismatches 64; Indels 24; Gaps 6;

Qy 1 MARGKIEIKLIENQTRQVYTKRRNGIFPKAQLTVLCDAKVSLMTNTKMGHEYISP 60
Db 1 MGRKIEIKRIENATNRQVYTKRRNGIMKKARELVLCDAQVALIFSSSTGKXHEFCSP 60

Qy 61 TTTTSMVDDYQKTMGIDLWRTHEESKDTLMKKEINNKLRREIRORLGHDLNGLSFDE 120
Db 61 STDKIGFDREYQQAIGTSLWIEQYENMQRTLSHLKQINRGIRFIRQRMGEDLDGDFDE 120

Qy 121 LASIDDEMOSLDAIRORXHVITKTQETTTKKVKNLEQRGMMLHGFDQBAAG--EPP 174
Db 121 LRGLQNVDAALKEVRHRKXHVITQETTTKKVKNLEQRGMMLHGFDQBAAG--EPP 170

Qy 175 QYGYEDNEGDIYBSALALNSGANLYTFHL--HHPNLHGGSSLSGSSITLHDLRL 231
Db 171 REEPAGFVNTGGWGDGAGAGAAADMAFAFRVPSQPNLH--GMAVGGN-----HDLRL 223

Search completed: September 27, 2004, 09:25:12
Job time : 93.3848 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:28:25 ; Search time 89.7897 Seconds
(without alignments)
830.848 Million cell updates/sec

Title: US-10-069-527-4

Perfect score: 1216
Sequence: 1 MARGKIKIKIENOTNRQVT.....HGGSSLSGSIITLHDLRLA 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	709.5	58.3	227	14	US-10-104-580-4
2	655.5	53.9	241	12	US-10-425-114-44825
3	652	53.6	260	12	US-10-425-114-39286
4	640.5	52.7	261	12	US-10-425-114-46248
5	631.5	51.9	243	12	US-10-424-599-209491
6	604.5	49.7	227	12	US-10-424-599-263636
7	576.5	47.4	223	12	US-10-425-114-42492
8	557	45.8	234	12	US-10-424-599-263637
9	474	39.0	143	12	US-10-425-114-41663
10	398	32.7	186	16	US-10-437-963-132081
11	383	31.5	208	12	US-10-424-599-208168
12	383	31.5	209	12	US-10-425-114-407939
13	373.5	30.7	207	12	US-10-424-599-175060
14	368.5	30.3	205	12	US-10-425-114-39944
15	331.5	27.3	208	12	US-10-412-6998-56

16	310	25.5	235	16	US-10-437-963-120366	Sequence 120366,
17	310	25.5	260	16	US-10-437-963-113197	Sequence 113197,
18	305.5	25.1	240	9	US-09-970-624-2	Sequence 2, Appl1
19	301	24.8	228	12	US-10-425-114-66169	Sequence 66169, A
20	301	24.8	289	16	US-10-437-963-173987	Sequence 173987,
21	297	24.4	189	16	US-10-437-963-153788	Sequence 153788,
22	296.5	24.4	221	12	US-10-412-699B-1728	Sequence 1728, Ap
23	295.5	24.3	249	12	US-10-425-114-54913	Sequence 54913, A
24	295.5	24.3	249	12	US-10-425-114-56968	Sequence 56968, A
25	295.5	24.3	249	12	US-10-425-114-61531	Sequence 61531, A
26	295.5	24.3	249	12	US-10-425-114-72229	Sequence 72229, A
27	295.5	24.3	288	12	US-10-425-114-42198	Sequence 42198, A
28	295.5	24.3	298	12	US-10-425-114-42117	Sequence 42117, A
29	291	23.9	233	12	US-10-425-114-39851	Sequence 39851, A
30	290.5	23.9	238	10	US-09-934-455-8	Sequence 8, Appl1
31	290.5	23.9	238	12	US-10-412-699B-68	Sequence 68, Appl
32	290.5	23.9	238	12	US-10-225-066A-328	Sequence 328, App
33	290.5	23.9	238	14	US-10-286-264-34	Sequence 34, Appl
34	290.5	23.9	238	15	US-10-374-780A-14	Sequence 14, Appl
35	290.5	23.9	282	12	US-10-424-599-156275	Sequence 156275,
36	288.5	23.7	228	10	US-09-819-142-4	Sequence 4, Appl1
37	288.5	23.7	228	12	US-09-934-455-32	Sequence 32, Appl
38	288.5	23.7	228	12	US-10-412-699B-938	Sequence 938, App
39	287	23.6	241	12	US-10-425-114-67499	Sequence 67499, A
40	287	23.6	247	12	US-10-425-114-40879	Sequence 40879, A
41	287	23.6	283	12	US-10-425-114-39568	Sequence 39568, A
42	287	23.6	283	12	US-10-425-114-56979	Sequence 56979, A
43	287	23.6	283	12	US-10-425-114-56989	Sequence 56989, A
44	287	23.6	292	12	US-10-425-114-39538	Sequence 39538, A
45	286.5	23.6	245	12	US-10-424-599-201348	Sequence 201348,

ALIGNMENTS

RESULT 1
US-10-104-580-4
; Sequence 4, Application US/10104580
; Publication No. US20030033628A1
GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-10-104-580-4
Query Match 58.3%; Score 709.5; DB 14; Length 227;
Best Local Similarity 62.3%; Pred. No. 9.1e-59;
Matches 149; Conservativity 24; Mismatches 45; Indels 21; Gaps 5;
Cy 1 MARGKIKIKIENOTNRQVTYSRRNGIFPKAQLTVLDCAVSLIMLNTKMHYISP 60
Db 1 MARGKIKIKIENPTNRQVTYSRRNGIFPKAQLTVLDCAVSLIMLNTKMHYISP 60
Cy TTTKSMYDDYQKMGIDLWRTHBSMKDTLWKLEINKKRREIFORGHDLNGISFPE 120
Db TTTKSMYDDYQKMGIDLWRTHBSMKDTLWKLEINKKRREIFORGHDLNGISFPE 120
Cy STSTKXIVQYQVAGIDIDMGTOYEMKQEHKLKNDINKLQCEIRORGBGINDLSI 120
Db STSTKXIVQYQVAGIDIDMGTOYEMKQEHKLKNDINKLQCEIRORGBGINDLSI 120
Cy 121 LASIDEMQSLDAIRQRKRVHVKIQTETTKKKVKVLEQRGRNMLHGYDQBAAGDP 180
Db 121 LASIDEMQSLDAIRQRKRVHVKIQTETTKKKVKVLEQRGRNMLHGYDQBAAGDP 180

Db 121 LRGLECHMTALNGVGRKXHVITKQNETYRKVKYKNLEERHGNLMNEY---EAKLEDROQ 177
Qy 161 GYEENEDYSSALALNSGANNLYTFELH-----PNIHHGSSISGSIHLHLRL 231
Db 178 GLVDN---EAAVALANGASLYAFRLHGHNNHHHLPLHL-GDGFGA-----HELRL 226

RESULT 2

US-10-425-114-44825
Sequence 44825, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 44825
LENGTH: 241
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701209467_FLI.pep
US-10-425-114-44825

Query Match 53.9%; Score 655.5; DB 12; Length 241;
Best Local Similarity 59.2%; Pred. No. 1.3e-53;
Matches 142; Conservative 32; Mismatches 51; Indels 15; Gaps 7;

Qy 1 MARGKIKIKLENTNQVYTSKRNGIFPKAQLTLCAPAKYSLMLSTNMGHEYISP 60
Db 9 MGRGKIKIKLENTNQVYTSKRNGIFPKAHLSTLCAPAKSLMPSKNNKHEYISP 68
Qy 61 TTTTSMYDDYQKTMG-IDLWRTHEESMKTLMKLEINNKLRREIRQRLGH--DLNGLS 117
Db 69 GLTTKRIIDYQKTLGIDLMHSHYEKMLENLKLLIDINNKLRRQIRHRIGEGLDMDWS 128
Qy 118 FDELASIDDEMOSSLDAIRQKXHVITQETETTKKKYKNLEQRGNMLHGYFPOEAAGED 177
Db 129 FOQLRTLEEDVSSIGIKRERKRFVITKRTDTCRKVKSLKQNNRDL--FELECAIH 185
Qy 178 PÖGYEDNEGDYESALALNSGANNLYTF-ELHHPNL-----HHGSSISGSIHLHLRL 232
Db 186 PÖFILHD-EGDEESAAVALANGASTLVAFCHGHSHNLPLPSH---SHGEPPFTDLDRLA 241

RESULT 3

US-10-425-114-39286
Sequence 39286, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39286
LENGTH: 260

TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3049-050-F6_FLI.pep
US-10-425-114-39286

Query Match 53.6%; Score 652; DB 12; Length 260;
Best Local Similarity 57.9%; Pred. No. 3e-53;
Matches 143; Conservative 31; Mismatches 53; Indels 20; Gaps 8;

Qy 1 MARGKIKIKLENTNQVYTSKRNGIFPKAQLTLCAPAKYSLMLSTNMGHEYISP 60
Db 19 MGRGKIKIKLENTNQVYTSKRNGIFPKAHLSTLCAPAKSLMPSKNNKHEYISP 78
Qy 61 TTTTSMYDDYQKTMG-IDLWRTHEESMKTLMKLEINNKLRREIRQRLGH--DLNGLS 117
Db 79 GLTTKRIIDYQKTLGIDLMHSHYEKMLENLKLLIDINNKLRRQIRHRIGEGLDMDWS 138
Qy 118 FDELASIDDEMOSSLDAIRQKXHVITQETETTKKKYKNLEQRGNMLHGYFPOEAAGED 177
Db 139 FOQLRTLEEDVSSIGIKRERKRFVITKRTDTCRKVKSLKQNNRDL--LELEKCVIH 195
Qy 178 PÖGYEDNEGDYES-----ALALNSGANNLYTF-ELHHPNL-----HHGSSISGSIHL 225
Db 196 PÖFILHD-EGDEESAAAAAVALANGASTLVAFCHGHSHNLPLPSHSGNGEPPFTD 254
Qy 226 LHLRLA 232
Db 255 -HLRLA 260

RESULT 4

US-10-425-114-46248
Sequence 46248, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 46248
LENGTH: 261
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701148021_FLI.pep
US-10-425-114-46248

Query Match 52.7%; Score 640.5; DB 12; Length 261;
Best Local Similarity 57.5%; Pred. No. 3.7e-52;
Matches 142; Conservative 31; Mismatches 55; Indels 19; Gaps 8;

Qy 1 MARGKIKIKLENTNQVYTSKRNGIFPKAQLTLCAPAKYSLMLSTNMGHEYISP 60
Db 19 MGRGKIKIKLENTNQVYTSKRNGIFPKAHLSTLCAPAKSLMPSKNNKHEYISP 78
Qy 61 TTTTSMYDDYQKTMG-IDLWRTHEESMKTLMKLEINNKLRREIRQRLGH--DLNGLS 117
Db 79 GLTTKRIIDYQKTLGIDLMHSHYEKMLENLKLLIDINNKLRRQIRHRIGEGLDMDWS 138
Qy 118 FDELASIDDEMOSSLDAIRQKXHVITQETETTKKKYKNLEQRGNMLHGYFPOEAAGED 177
Db 139 FOQLRTLEEDVSSIGIKRERKRFVITKRTDTCRKVKSLKQNNRDL--KEKCVIH 196
Qy 178 PÖGYEDNEGDYES-----ALALNSGANNLYTF-ELHHPNL-----HHGSSISGSIHL 225

Page 3

Query Match	47.4%	Score 576.5	DB 12	Length 223
Best Local Similarity	50.5%	Pred. No. 3.3e-46		
Matches 112	Conservative 40	Mismatches 63	Indels 7	Gaps 3

QY	5	KIEIKLIENTONTROYTSKRRNGIFPKAQSITVCDKAVSLIMSNTHKQHEIYISPTTTT	64
Db	1	KIQIKRIENTNTROYTSKRRNGIFPKANEITVCDKAVSLIMSSGTHKHEIYISPTST	60
QY	65	KSNWDDYQKTMGIDLMFTHEESMDLTMLKKEIINNKARRERISQSLGHDLNGISFDELAST	124
Db	61	KQFPDQYQMTLGVDLNMSHYENMOENLKLKDVVRNRIRKEIRQMGDCINDLGHEDLKL	120
QY	125	DDMOSSLDAIRQRKHVIRKQETTTKKYKYNLEQRGRNMLHGYPDQEAQEDDPQGYED	184
Db	121	EEENDKAKAVVRERKYYKVINQIDTQGRKKENNEKEVHNRLIR---DIDARAEDPRFALID	177
QY	185	NEGDPYSALALNSGANNLYTFPHLH--HPNLIHGGSSLSGSSIT	224
Db	178	NGGEYESVIGFNSUGPRKFAFLSLQPSRPSAQSGAA--GSDIT	217

RESULT 8
 US-10-424-599-263637
 ; Sequence 263637, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 263637
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1.pep
 US-10-424-599-263637

Query Match 45.8%; Score 557, DB 12; Length 234;
 Best Local Similarity 48.1%; Pred. No. 2.5e-44;
 Matches 112; Conservative 41; Mismatches 66; Indels 14; Gaps 4;

QY 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAOELTVLCAKYSILMLSTNKKHEIYSP 60
 DB 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAOELTVLCAKYSILMLSTNKKHEIYSP 60
 QY 61 TTTKSMYDDYQXTMGIDLMRTHEESMKDLMKLEINNKLRREIRQRLGHDINGLSFDE 120
 DB 61 STTKQFPDQYQMTLGVDLNMSHYENMQENLKKLVNRRLRKEIRQMGDCINDLGMD 120
 QY 121 LASIDDEMOSSLDAIRQK-----KXHVIKTQETTTKKVKVRLQGRGNNLHGYPDQA 173
 DB 121 LKLEEMDMDAKAVRERSCTWRKQKHTVRIIVQRKKFNKEKVENRLLE--DIDA 177
 QY 174 AGEDPQYGEDNEGYESALALNSGANNLYTFHLH--HPNLHHGSSSLGSSIT 224
 DB 178 RAEDPRRALIDNGEYEVSVIGFSLGPRFALSLQSHPSAGGAA--GSDLT 228

RESULT 9
 US-10-425-114-41663
 ; Sequence 41663, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 41663
 ; LENGTH: 143
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: jC-gmf102220148g99_FLI.pep
 US-10-425-114-41663

Query Match 39.0%; Score 474; DB 12; Length 143;
 Best Local Similarity 62.6%; Pred. No. 8.8e-37;
 Matches 87; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAOELTVLCAKYSILMLSTNKKHEIYSP 60
 DB 4 MARGKIEIKLENOTNROVYTSKRNGIFKKAOELTVLCAKYSILMLSTNKKHEIYSP 63
 QY 61 TTTKSMYDDYQXTMGIDLMRTHEESMKDLMKLEINNKLRREIRQRLGHDINGLSFDE 120
 DB 64 STTKQFPDQYQMTLGVDLNMSHYENMQENLKKLVNRRLRKEIRQMGDCINDLGMD 123
 QY 121 LASIDDEMOSSLDAIRQK 139
 DB 124 LKLEEMDMDAKAVRERK 142

RESULT 10
 US-10-437-963-132081
 ; Sequence 132081, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Batbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437, 963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 132081
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_34084C.1.pep
 US-10-437-963-132081

Query Match 32.7%; Score 398; DB 16; Length 186;
 Best Local Similarity 41.0%; Pred. No. 1.9e-29;
 Matches 98; Conservative 29; Mismatches 50; Indels 62; Gaps 9;

QY 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAOELTVLCAKYSILMLSTNKKHEIYSP 60
 DB 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAOELTVLCAKYSILMLSTNKKHEIYSP 54
 QY 61 TTTKSMYDDYQXTMGIDLMRTHEESMKDLMKLEINNKLRREIRQRLGHDINGLSFDE 120
 DB 55 ---KGIDRYQQAIGTSLMIS-----QRMGEDLDGLEFDE 87
 QY 121 LASIDDEMOSSLDAIRQKXHVIKTQETTTKKVKVRLQGRGNNLHGYPDQA 174
 DB 88 LRLEQNVDAAL-----KEYVITQTETVKKVY-----HSYEAYETLQDELGL 132
 QY 175 GEDPQYGEDNEGYESALALNSGANNLYTFHLH--HPNLHHGSSSLGSSITLHDLRL 231
 DB 133 REEPAGFVDNTGGGMDGAGAAADMFARVVPSQPNLH--GMAVGN---HDLRL 185

RESULT 11
 US-10-424-599-208168
 ; Sequence 208168, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 208168
LENGTH: 208
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_2C.1.pep
US-10-424-599-208168

Query Match 31.5%; Score 383; DB 12; Length 208;
Best Local Similarity 38.8%; Pred. No. 5.8e-28;
Matches 83; Conservative 43; Mismatches 76; Indels 12; Gaps 3;

QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFKKAQELTVLCAKVSLLMLSTNKKHEIYISP 60
DB 1 MGRGKIEIKRIENSNRQVTSKRRNGILKKAKEITVLCDAQVSLIIFASGKHDYISP 60
QY 61 TTTTSMYDDYQKTWIGIDIMRTHESMKDTLWKKEINNKLRREIRQRLGHDINGLSFDE 120
DB 61 STTILDLIRYHKTSGKRLMDAKHENLNGEIERLKENDSQWIELRHLKGDIDINSINYKE 120
QY 121 LASTIDEMOSSLDALRQRKHVITKQTETTKKKVKNLEQRGNMLHGVPQEAAGEPQY 180
DB 121 LMALEDALLETGLVSRKQMDVYRMLR--NDKILBEENRELNPLMOORLAEGAREVDN 178
QY 181 GYEDNEGDEYESALALSGANNLYTFHLH--HPNL 212
DB 179 GFDQSVRDYNSHMP-----FAFRVQPMQPNL 204

RESULT 12
US-10-425-114-40799
Sequence 40799, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40799
LENGTH: 209
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3030-006-DB_FLI.pep
US-10-425-114-40799

Query Match 31.5%; Score 383; DB 12; Length 209;
Best Local Similarity 38.8%; Pred. No. 5.9e-28;
Matches 83; Conservative 43; Mismatches 76; Indels 12; Gaps 3;

QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFKKAQELTVLCAKVSLLMLSTNKKHEIYISP 60
DB 2 MGRGKIEIKRIENSNRQVTSKRRNGILKKAKEITVLCDAQVSLIIFASGKHDYISP 61
QY 61 TTTTSMYDDYQKTWIGIDIMRTHESMKDTLWKKEINNKLRREIRQRLGHDINGLSFDE 120
DB 61 STTILDLIRYHKTSGKRLMDAKHENLNGEIERLKENDSQWIELRHLKGDIDINSINYKE 121
QY 121 LASTIDEMOSSLDALRQRKHVITKQTETTKKKVKNLEQRGNMLHGVPQEAAGEPQY 180
DB 121 LMALEDALLETGLVSRKQMDVYRMLR--NDKILBEENRELNPLMOORLAEGAREVDN 179

QY 181 GYEDNEGDEYESALALSGANNLYTFHLH--HPNL 212
DB 180 GFDQSVRDYNSHMP-----FAFRVQPMQPNL 205

RESULT 13
US-10-424-599-175060
Sequence 175060, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175060
LENGTH: 207
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(207)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_129098C.1.pep
US-10-424-599-175060

Query Match 30.7%; Score 373.5; DB 12; Length 207;
Best Local Similarity 37.7%; Pred. No. 4.6e-27;
Matches 81; Conservative 45; Mismatches 74; Indels 15; Gaps 3;

QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFKKAQELTVLCAKVSLLMLSTNKKHEIYISP 60
DB 1 MGRGKIEIKRIENSNRQVTSKRRNGILKKAKEISVLCDAQVSLIIFVSGKHEIYISP 60
QY 61 TTTTSMYDDYQKTWIGIDIMRTHESMKDTLWKKEINNKLRREIRQRLGHDINGLSFDE 120
DB 61 STTILDLIRYHKTSGKRLMDAKHENLNGEIERLKENDSQWIELRHLKGDIDITSINYKE 120
QY 121 LASTIDEMOSSLDALRQRKHVITKQTETTKKKVKNLEQRGNMLHGVPQEAAGEPQY 177
DB 121 LMALEDALLETGLVSRKQMDVYRMLR--MFKNDKILBEENRELNPLMOORLAEGAREVDN 176
QY 178 PCYGEDNEGDEYESALALSGANNLYTFHLHHPNL 212
DB 177 MONGFNEIKRVFNSHMQRAAS-----LKQPNL 203

RESULT 14
US-10-425-114-39944
Sequence 39944, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39944
LENGTH: 205
TYPE: PRT

```

/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700903463_FLI.pep
US-10-425-114-39944

Query Match          30.3%; Score 368.5; DB 12; Length 205;
Best Local Similarity 42.1%; Pred. No. 1.3e-26;
Matches 77; Conservative 37; Mismatches 48; Indels 21; Gaps 3;

QY 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKGHEIYSP 60
DB 25 MGRGKIEIKRIENSNNQVYTSKRNGILTKAKEISVLCDQVSLIFVSGMGHEIYSP 84
QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKDTLMKLEINNKLRREIRQRGLDNGLSFDE 120
DB 85 STTIDVLDYQKSGKTLMDAKHENLSNEIDRIKENDSMQLELHKLGEEDITSILNYKE 144
QY 121 LASLDDMQSSLDLAIROKXYHVIKTQETETKKKVKNLDEGR-----GNN 164
DB 145 LMALEDLLEHGLDVKVRHQMEILSKRNRNEMVAEBQRQLTFQDQCEMAIASNAGMM 200
QY 165 LKG 167
DB 201 -HG 202

RESULT 15
US-10-412-699B-56
/ Sequence 56, Application US/10412699B
/ Publication No. US2004045049A1
/ GENERAL INFORMATION:
/ APPLICANT: Mendel Biotechnology, Inc.
/ APPLICANT: Zhang, James
/ APPLICANT: Fromm, Michael E.
/ APPLICANT: Heard, Jacqueline E.
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Adam, Luc J.
/ APPLICANT: Broun, Pierre E.
/ APPLICANT: Pineda, Omalra
/ APPLICANT: Reuber, T. Lynne
/ APPLICANT: Keddie, James S.
/ APPLICANT: Yu, Quo-liang
/ APPLICANT: Uiang, Cai-Zhong
/ APPLICANT: Samaha, Raymond R.
/ APPLICANT: Pilgram, Marsha L.
/ APPLICANT: Creelman, Robert A.
/ APPLICANT: DuBell, Arnold N.
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Kimimoto, Roderick
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
/ FILE REFERENCE: MBI-0048CIP
/ CURRENT APPLICATION NUMBER: US/10/412,699B
/ PRIOR FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: 09/394,519
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: 09/489,376
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: 09/506,720
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 09/533,030
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,392
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,029
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/532,591
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/533,648
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: 09/713,994
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 09/819,142

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/ PRIOR FILING DATE: 2001-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 56
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ OTHER INFORMATION: G134
US-10-412-699B-56

Query Match          27.3%; Score 331.5; DB 12; Length 208;
Best Local Similarity 36.0%; Pred. No. 4.3e-23;
Matches 71; Conservative 39; Mismatches 64; Indels 23; Gaps 3;

QY 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKGHEIYSP 60
DB 1 MGRGKIEIKRIENANNRVTFPSKRRNGILYKAKEITVLCDQKVALIFASNGKMIDYCCP 60
QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKDTLMKLEINNKLRREIRQRGLDNGLSFDE 120
DB 61 SMDLGAMLDQYQKSGKTLMDAKHENLSNEIDRIKENDSLQELHKLGEEDITSILNYKE 120
QY 121 LASLDDMQSSLDLAIROKXYHVIKTQETETKKKVKNLDEGR-----RGNNL 165
DB 121 LMAVEHAIENGLDVKVRHQMEILSKRNRNEMVAEBQRQLTFQDQCEMAIASNAGMM 180
QY 166 HGFPDQAPAGDPQYCY 182
DB 181 RDH-----DQDFGY 189

Search completed: September 27, 2004, 09:44:50
Job time : 90.7897 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:19:49 / Search time 25.9508 Seconds
(without alignments)
859.952 Million cell updates/sec

Title: US-10-069-527-4

Perfect score: 1216
Sequence: 1 MARCKIRIKIENQTNROVT.....HGGSSISGSIHLHLRLA 232

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696.5	57.3	222	2 S23731	MADS box protein T
2	667.5	54.9	227	2 S23738	MADS box protein d
3	641.5	52.8	231	2 S31693	MADS box protein g
4	628.5	51.7	228	2 T07066	MADS box protein h
5	624.5	51.4	228	2 T07410	MADS box protein h
6	620.5	51.0	229	2 T09335	MADS-box protein h
7	564	46.4	232	2 A42095	floral homeotic pr
8	558.5	45.9	224	2 T14473	MADS box protein 2
9	549	45.1	214	2 T10715	MADS box protein c
10	544.5	44.8	224	2 T14474	MADS box protein c
11	500.5	41.2	203	2 T06277	MADS box protein a
12	385	31.7	212	2 S31707	floral homeotic pr
13	385	31.7	212	2 S60268	FBP3 protein - gar
14	347.5	28.6	215	2 S28086	homeotic protein g
15	340.5	28.0	209	2 S35226	homeotic protein g
16	331.5	27.3	210	2 A53839	B function floral
17	326	26.8	210	2 U01689	floral binding pro
18	313	25.7	210	2 T03902	MADS4 box protein
19	306.5	25.2	209	2 T03894	MADS box protein -
20	301	24.8	249	2 T04335	MADS box protein -
21	298	24.5	229	2 T04307	M79 protein - rice
22	296.5	24.4	221	2 T09347	MADS box protein A
23	295	24.3	251	2 T04169	MADS box protein -
24	291	23.9	231	2 T14801	MADS box protein W
25	288.5	23.7	228	2 T05621	MADS-box protein A
26	287	23.6	248	2 T04170	MADS box protein -
27	283.5	23.3	224	2 J01690	MADS box protein f
28	281	23.1	227	2 H04614	probable MADS-box
29	281	23.1	250	2 T04167	MADS box protein -

30	280.5	23.1	247	2 S78015	MADS box protein D
31	280.5	23.1	250	2 D39534	MADS box protein A
32	280.5	23.1	251	2 T00656	MADS box protein A
33	280.5	23.1	256	2 T45817	MADS transcription
34	280.5	23.1	261	2 T09603	MADS-box protein 3
35	280	23.0	242	2 S71208	MADS box protein 3
36	280	23.0	246	2 T17023	MADS box protein A
37	280	23.0	252	2 F39534	floral homeotic pr
38	280	23.0	254	2 T10467	MADS box protein D
39	279.5	22.9	261	2 S51935	probable MADS-box
40	279	22.9	246	2 E39534	floral homeotic pr
41	279	22.9	248	2 S20886	MADS box protein b
42	279	22.9	258	2 G84858	floral homeodomain
43	278	22.9	262	2 T08039	MADS-box protein -
44	277.5	22.8	243	2 S71756	MADS box protein D
45	277	22.8	233	2 T10714	MADS-box protein C

ALIGNMENTS

RESULT 1

S23731 MADS box protein TDR6 - tomato (fragment)

N/Alternate names: floral homeotic protein TM6

C/Species: Lycopersicon esculentum (tomato)

C/Date: 27-May-1994 #sequence_revision 26-May-1995 #text_change 26-Aug-1995

C/Accession: S23731, S38778

R/Pnueli, L.; Abu-Abeid, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschultz, E.

Plant J. 1, 255-266, 1991

A/Title: The MADS box gene family in tomato: temporal expression during floral development

A/Reference number: S23728, PMID:93251098, PMID:1688249

A/Accession: S23731

A/Molecule type: mRNA

A/Residues: 1-222 <PNU>

A/Cross-references: EMBL:X60759

R/Pnueli, L.

submitted to the EMBL Data Library, July 1991

A/Reference number: S38778

A/Accession: S38778

A/Molecule type: mRNA

A/Residues: 1-159, 'T', 161-222 <PNU>

A/Cross-references: EMBL:X60759, NID:g19385, PID:g19386

C/Genetics:

A/Map position: 2

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homolog

C/Keywords: DNA binding; nucleus; transcription regulation

F,1-54/Domain: serum response factor DNA-binding domain homology (fragment) <SRP>

Query Match 57.3%; Score 696.5; DB 2; Length 222;

Best local similarity 60.2%; Pred. No. 7,7e-43;

Matches 139; Conservative 29; Mismatches 52; Indels 11; Gaps 4;

RESULT 2

S12378 MADS box protein defa-1 - garden snapper

N/Alternate names: gene deficiencies protein
 C/Species: Antirrhinum majus (garden snapdragon)
 C/Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
 C/Accession: S12378; S19232
 R/Schwarz-Sommer, H.; Beltrami, J.P.; Huijser, P.; Pape, H.; Loeonig, W.E.; Siedler, H.; Schwarz-EMBO J. 9, 605-613, 1990
 A/Title: Deficiens, a homeotic gene involved in the control of flower morphogenesis in A
 A/Reference numbers: S12378; MUID:90183955; PMID:1568830
 A/Accession: S12378
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-227 <SOM>
 A/Cross-references: GB:X52023; NID:916019; PIDN:CAA36268.1; PID:916020
 R/Schwarz-Sommer, Z.; Hue, I.; Huijser, P.; Flor, P.J.; Hansen, R.; Tietens, F.; Loeonig, EMBO J. 11, 221-263, 1992
 A/Title: Characterization of the Antirrhinum floral homeotic MADS-box gene deficiencies: ev
 A/Reference number: S19232; MUID:92155166; PMID:1346760
 A/Accession: S19232
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-227 <SCH>
 A/Cross-references: EMBL:X62810; NID:916017; PIDN:CAA44629.1; PID:916018
 C/Genetics:
 A/Gene: deficiencies
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; nucleus; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 54.9%; Score 667.5; DB 2; Length 227;
 Best Local Similarity 56.4%; Pred. No. 9.3e-41;
 Matches 128; Conservative 37; Mismatches 53; Indels 9; Gaps 3;

1 MARGKIEIKLENOTNRQVYTSKRRNGIFPKAQLTVLCAKYSILMLSTNRQHEHYISP 60
 1 MARGKIQIKRIENOTNRQVYTSKRRNGIFPKAQLTVLCAKYSILMLSTNRQHEHYISP 60

QY 61 TTTKSMYDDYQKTMGIDLWRTHEBSMKDTLWTKKINRKLREIRORLGHDLNGLSFDE 120
 DB 61 TTTATKQFLDQYQKAVGVDLWSSHYEKQKQELKLNENRNLREIRORMESLNDLYEQ 120

QY 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKYKVLQORGNMLHGYFDOBAAGDPQY 180
 DB 121 TVNLIEVDNSLKLIRKRVKIVSNQIDYSKKVKNVVEIHRNLV--LEFDARQEDP 177

QY 181 GYEDNEGDYSSALALSGANNLYTFHL--HHPNHLHGSSLGSSIT 224
 DB 178 GLVDEGDYNSVLFPGNGRRIALRLPNNHPTLHSG--GSDLT 221

RESULT 3
 S31693
 MADS box protein gp - garden petunia
 N/Alternate names: floral homeotic protein gp; transcription factor gp
 C/Species: Petunia x hybrida (garden petunia)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Sep-1999
 C/Accession: S31693
 R/Kush, A.; Brumelle, A.; Shevell, D.; Chua, N.H.
 submitted to the EMBL Data Library, November 1992
 A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS box
 A/Reference number: S31693
 A/Accession: S31693
 A/Molecule type: mRNA
 A/Residues: 1-231 <KUS>
 A/Cross-references: EMBL:X69946; NID:922664; PID:922665
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 52.8%; Score 641.5; DB 2; Length 231;
 Best Local Similarity 55.6%; Pred. No. 6.9e-39;
 Matches 129; Conservative 36; Mismatches 52; Indels 15; Gaps 4;

QY 1 MARGKIEIKLENOTNRQVYTSKRRNGIFPKAQLTVLCAKYSILMLSTNRQHEHYISP 60
 DB 1 MARGKIQIKRIENOTNRQVYTSKRRNGIFPKAQLTVLCAKYSILMLSTNRQHEHYISP 60

QY 61 TTTKSMYDDYQKTMGIDLWRTHEBSMKDTLWTKKINRKLREIRORLGHDLNGLSFDE 120
 DB 61 TTTATKQFLDQYQKAVGVDLWSSHYEKQKQELKLNENRNLREIRORMESLNDLYEQ 120

QY 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKYKVLQORGNMLHGYFDOBAAGDPQY 180
 DB 121 TVNLIEVDNSLKLIRKRVKIVSNQIDYSKKVKNVVEIHRNLV--LEFDARQEDP 176

QY 181 GYEDNEGDYSSALALSGANNLYTFHL--HHPNHLHGSSLGSSIT 224
 DB 177 GLVEGDYNSVLFPGNGRRIALRLPNNHPTLHSG--GSDIT 225

RESULT 4
 T07066
 MADS-box protein homolog DEF4 - potato
 N/Alternate names: deficiencies analogue
 C/Species: Solanum tuberosum (potato)
 C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
 C/Accession: T07066
 R/Garcia-Maroto, F.; Salami, F.; Rohde, W.
 Plant J. 4, 771-780, 1993
 A/Title: Molecular cloning and expression patterns of three alleles of the Deficiens-hom
 A/Reference number: Z15896; MUID:94100991; PMID:7903890
 A/Accession: T07066
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-228 <GAR>
 A/Cross-references: EMBL:X67511; NID:9431225; PIDN:CAA47846.1; PID:9431226
 A/Experimental source: cv. Granola; leaf
 A/Gene: def4
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 51.7%; Score 628.5; DB 2; Length 228;
 Best Local Similarity 54.1%; Pred. No. 5.6e-38;
 Matches 124; Conservative 40; Mismatches 54; Indels 11; Gaps 3;

1 MARGKIEIKLENOTNRQVYTSKRRNGIFPKAQLTVLCAKYSILMLSTNRQHEHYISP 60
 1 MARGKIQIKRIENOTNRQVYTSKRRNGIFPKAQLTVLCAKYSILMLSTNRQHEHYISP 60

QY 61 TTTKSMYDDYQKTMGIDLWRTHEBSMKDTLWTKKINRKLREIRORLGHDLNGLSFDE 120
 DB 61 SITTKQFLDQYQKAVGVDLWSSHYEKQKQELKLNENRNLREIRORMESLNDLYEQ 120

QY 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKYKVLQORGNMLHGYFDOBAAGDPQY 180
 DB 121 LELMEVDNSLKLIRKRVKIVGNQETETTKKKYKVLQORGNMLHGYFDOBAAGDPQY 177

QY 181 GYEDNEGDYSSALALSGANNLYTFHL--HHPNHLHGSSLGSSIT 224
 DB 178 GLVEGDYNSVLFPGNGRRIALRLPNNHPTLHSG--GSDIT 223

RESULT 5
 T07410
 MADS box protein homolog DEF2 - potato
 N/Alternate names: deficiencies analogue
 C/Species: Solanum tuberosum (potato)
 C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 03-Dec-1999
 C/Accession: T07410
 R/Garcia-Maroto, F.
 submitted to the EMBL Data Library, August 1992
 A/Reference number: Z16019
 A/Accession: T07410

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-228 <GAR>
 A:Cross-references: EMBL:X67508; NID:G511064; PIDN:CAA47845.1; PID:G511065
 A:Experimental source: cv. H81.1506/60; dev. stage vegetative; tissue type flower
 C:Genetics:
 A:Gene: def2
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 51.4%; Score 624.5; DB 2; Length 228;
 Best Local Similarity 53.7%; Pred. No. 1.1e-37;
 Matches 123; Conservative 41; Mismatches 54; Indels 11; Gaps 3;

QY 1 MARGKIEIKLENTNRQVTSKRRNGIFPKAOELTVLCAKVSILMLNTNKHETISP 60
 DB 1 MARGKIQIKLENTNRQVTSKRRNGIFPKANELTVLCAKVSIMWISSGKHEITSP 60
 QY 61 TTTTSMYDYQKTWIGIDLMRTHEESMKDTLWKLEINNKLRREIRQLGHDINGLSFDE 120
 DB 61 SITNNLEPDLQKTIQVDMTSHYERKQEQRLKLDVVRNLRKEIRORMGESLNDLNFQ 120
 QY 121 LASLDEMOSSLDALRQRKHVITKQTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 180
 DB 121 LEELEMDVNSLKLIREKRYVIGNQLETYRKVRNVEIHRNL--LEFDARQEDPYG 177
 QY 181 GYEDNEGDEYSALALNSGANNLYTFHL-----HHPNLHGSSSGSSIT 224
 DB 178 GLVNGEDGYNSVLGPRPGCHHILALGLQPNNNHHHLSGSG--GSDIT 223

RESULT 6
 T09335
 MADS-box protein NMH 7 - alfalfa
 C:Species: Medicago sativa (alfalfa)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Dec-1999
 C:Accession: T09335
 R:Kilby, C.; Heard, J.; Carroll, S.; Leshner, J.; Ganter, G.; Dunn, K.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z16647
 A:Accession: T09335
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-229 <KIR>
 A:Cross-references: EMBL:AF042068; NID:G2827299; PID:G2827300
 A:Experimental source: strain Iroquois; root nodules
 C:Genetics:
 A:Gene: nmh 7
 A:Insertions: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C:Keywords: DNA binding; transcription regulation
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 51.0%; Score 620.5; DB 2; Length 229;
 Best Local Similarity 54.0%; Pred. No. 2.2e-37;
 Matches 122; Conservative 36; Mismatches 63; Indels 5; Gaps 2;

QY 1 MARGKIEIKLENTNRQVTSKRRNGIFPKAOELTVLCAKVSILMLNTNKHETISP 60
 DB 1 MARGKIQIKLENTNRQVTSKRRNGIFPKANELTVLCAKVSIMWISSGKHEITSP 60
 QY 61 TTTTSMYDYQKTWIGIDLMRTHEESMKDTLWKLEINNKLRREIRQLGHDINGLSFDE 120
 DB 61 SASLQPFQDYQMTVIGIDLMASHYENNGENLKKLDVVRNLRKEIRORMGESLNDLNFQ 120
 QY 121 LASLDEMOSSLDALRQRKHVITKQTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 180
 DB 121 LRLEDEMDKAKAIRERKYVITQIDTORKKSNNEBVRNRLR--DIDARAEPRF 177
 QY 181 GYEDNEGDEYSALALNSGANNLYTFHL--HHPNLHGSSSGSSIT 224
 DB 178 EMDNGEYEVSYGTSNIGPRMFLSLQPTHPNPNANGASASADLT 223

RESULT 7
 A42095
 floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
 N:Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A42095; S52633; T47593
 R:Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
 Cell 68, 683-697, 1992
 A:Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and its ex

A:Reference number: A42095; M01D:92154682; PMID:1346756
 A:Accession: A42095
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-232 <JAC>

A:Cross-references: GB:M6357; NID:G166607; PIDN:AAA32740.1; PID:G166608
 A:Experimental source: petals, stamens
 A:Note: Sequence extracted from NCBI Backbone (NCBI:82520, NCBI:82521)
 R:Okamoto, H.; Yano, A.; Shirahishi, H.; Okada, K.; Shimura, Y.
 Plant Mol. Biol. 26, 465-472, 1994
 A:Title: Genetic complementation of a floral homeotic mutation, apetal3, with an Arabid

A:Reference number: S52633; M01D:95036018; PMID:7948893.
 A:Accession: S52633
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-63 <OKA>
 A:Cross-references: GB:D21125
 R:Biocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.; Mewes,

submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24469
 A:Accession: T47593
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-232 <BLO>
 A:Cross-references: EMBL:AL132971
 A:Experimental source: cultivar Columbia; BAC clone T12E18
 C:Genetics:
 A:Map position: 3
 A:Insertions: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 A:Note: T12E18.30
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C:Keywords: DNA binding; nucleus; transcription regulation
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 46.4%; Score 564; DB 2; Length 232;
 Best Local Similarity 52.8%; Pred. No. 2.4e-33;
 Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGKIEIKLENTNRQVTSKRRNGIFPKAOELTVLCAKVSILMLNTNKHETISP 60
 DB 1 MARGKIQIKLENTNRQVTSKRRNGIFPKAHELTVLCAKVSIMWISSGKHEITSP 60
 QY 61 TTTTSMYDYQKTWIGIDLMRTHEESMKDTLWKLEINNKLRREIRQLGHDINGLSFDE 120
 DB 61 NTTTKEIVLQYTSIDVWATQYERMQETKRLTETNNRLTQIKRIGECIDELDIOE 120
 QY 121 LASLDEMOSSLDALRQRKHVITKQTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 180
 DB 121 LRLEDEMDKAKAIRERKYVITQIDTORKKSNNEBVRNRLR--EELRAEDPRY 177
 QY 181 GYEDNEGDEYSALALNSGANNLYTFHLHHPNLH 214
 DB 178 GLVNGEDGYNSVLGQIEGSRAYALRFHQ-NHHH 210

RESULT 8
 T14473
 MADS box protein 2AP3 - broccoli
 N:Alternate names: homeotic protein 2AP3
 C:Species: Brassica oleracea var. botrytis (broccoli)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

quely malcu

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:11:24 ; Search time 15.5705 Seconds
(without alignments)
775.845 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARGIKIKIENQTRQVT.....HHGSSLSGSSITLHDLRLA 232

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	667.5	54.9	227	1	DEFA_ANTWA
2	641.5	52.8	231	1	MAD1_PETTY
3	564	46.4	232	1	AP3_ARATH
4	549	45.1	214	1	CMB2_DIAA
5	385	31.7	212	1	MAD2_PETTY
6	350.5	28.8	237	1	M13_GNEGN
7	347.5	28.6	215	1	GLOB_ANTWA
8	340.5	28.0	209	1	GLOB_TOBAC
9	332	27.3	259	1	M17_MAIZE
10	331.5	27.3	208	1	P1ST_ARATH
11	326	26.8	210	1	F8P1_PETTY
12	320.5	26.4	252	1	TT16_ARATH
13	307	25.2	268	1	F824_PETTY
14	297.5	24.5	247	1	DE21_ANTWA
15	296.5	24.4	221	1	AG14_ARATH
16	295	24.3	241	1	AG19_PETTY
17	288.5	23.7	228	1	AG1Y_ARATH
18	285	23.4	265	1	JOIN_LYCES
19	283	23.3	241	1	AG18_SINLA
20	281	23.1	227	1	AG17_ARATH
21	280.5	23.1	250	1	SEB2_ARATH
22	280.5	23.1	251	1	SEP3_ARATH
23	280	23.0	242	1	AG18_ARATH
24	280	23.0	252	1	AG16_ARATH
25	280	23.0	254	1	AG19_SINLA
26	279	22.9	246	1	AG15_ARATH
27	277	22.8	233	1	CMB1_DIAA
28	276	22.7	268	1	AG15_ARATH
29	275.5	22.7	224	1	AG18_LYCES
30	275	22.6	227	1	AG18_LYCES
31	274	22.5	250	1	AG19_ARATH
32	271.5	22.3	251	1	SEP1_ARATH
33	270.5	22.2	253	1	CAL_ARATH

34	270	22.2	244	1	AG13_ARATH	Q38837 arabidopsis
35	269.5	22.2	242	1	SOCI_ARATH	Q64645 arabidopsis
36	269.5	22.2	242	1	AG_PANGI	Q40872 panax ginseng
37	268	22.0	258	1	AG13_ARATH	P29383 arabidopsis
38	267	22.0	219	1	AG19_ARATH	Q82743 arabidopsis
39	265	21.8	230	1	AG11_ARATH	Q38836 arabidopsis
40	265	21.8	248	1	AG11_ARATH	P29381 arabidopsis
41	264	21.7	250	1	AG18_SINLA	Q22328 solanum tub
42	262.5	21.6	250	1	AG18_SINLA	Q42429 solanum tub
43	261	21.5	248	1	AG_TOBAC	Q43585 nicotiana t
44	260.5	21.4	248	1	AG_LYCES	Q40168 lycopersico
45	260.5	21.4	252	1	AG_ARATH	P17839 arabidopsis

ALIGNMENTS

RESULT 1	DEFA_ANTWA	STANDARD;	PRT;	227 AA.
ID	DEFA_ANTWA			
AC	P23706;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Floral homeotic protein deficiencies.			
GN	DEFA.			
OS	Antirrhinum majus (Garden snapdragon).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiales; Lamiales; Antirrhinaceae; Antirrhineae; Antirrhinum.			
OX	NCBI_TaxID=4151;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90183955; PubMed=1968830;			
RA	Sommer H., Beltran J.-P., Huisser P., Pape H., Loeenig W.-E.,			
RA	Saedler H., Schwarz-Sommer Z.;			
RT	"Deficiens, a homeotic gene involved in the control of flower			
RT	morphogenesis in Antirrhinum majus: the protein shows homology to			
RT	transcription factors.";			
RL	EMBO J. 9:605-613(1990).			
RP	SEQUENCE FROM N.A.			
RC	STRATIN=cy. Sipe 50;			
RX	MEDLINE=9215166; PubMed=1346760;			
RA	Schwarz-Sommer Z., Hue I., Huisser P., Flor P.J., Hansen R.,			
RA	Teters F., Loeenig W.-E., Saedler H., Sommer H.;			
RT	"Characterization of the Antirrhinum floral homeotic MADS-box gene			
RT	deficiens: evidence for DNA binding and autoregulation of its			
RT	persistent expression throughout flower development.";			
RL	EMBO J. 11:251-263(1992).			
CC	- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF			
CC	FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH GLOBOSA (GLO).			
CC	- SUBCELLULAR LOCATION: Nuclear.			
CC	- INTO SEPARATE AND SPATIAL INTO CARPALS.			
CC	- SIMILARITY: Contains 1 MADS-box domain.			
CC	- SIMILARITY: Contains 1 MADS-box domain.			
CC	- This SWISS-PROT entry is copyrighted. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; X52023; CAA36268.1; -			
DR	EMBL; X62810; CAA4629.1; -			
DR	PIR; S12378; S12378.			
DR	HSSP; P11746; 1MM.			
DR	TRANSFAC; T01008; -			
DR	InterPro; IPR002487; TF_Kbox.			
DR	InterPro; IPR002100; TF_MADSbox.			

DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADS-DOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Developmental protein.
 FT DOMAIN 3
 FT DOKAIN 93 165 MADS-box.
 SQ SEQUENCE 227 AA; 26279 MW; 95E3FF60924FDEBD CRC64;
 Query Match 54.9%; Score 667.5; DB 1; Length 227;
 Best Local Similarity 56.4%; Pred. No. 6.6e-41;
 Matches 126; Conservative 37; Mismatches 53; Indels 9; Gaps 3;
 QY 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSILMLSTNKNMHEIYSP 60
 DB 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSILMLSTNKNMHEIYSP 60
 QY 61 TTTTSMYDYQKTMGIDLMRTHEESMKDTLWKLEINNKLRREIRQLGHDINGLSFDE 120
 DB 61 TTTTSMYDYQKTMGIDLMRTHEESMKDTLWKLEINNKLRREIRQLGHDINGLSFDE 120
 QY 121 LASIDDEMGSLLDAIRQKRVHVTQCTETTKKKYKNLEQRGMMLHGYPQEAAGEDPOY 180
 DB 121 IVNLIEMDNLSLKIRERKRVISNOIDTSKKKRVNVEIHRNLV--LEFDRARDDPAF 177
 QY 181 GYEDNEGYESALASNGANNLTFFHL--HHNLIHGGSSIGSSIT 224
 DB 178 GLVNEGDYNSVLGFPNGGRITALLRLPTNHHPTLHSGG--GSDIT 221
 RESULT 2
 ID MADI_PETHY STANDARD; PRT; 231 AA.
 AC C07472;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein PMADS 1 (Green petal homeotic protein).
 GN PMADS1 OR GP.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Petunia.
 ON NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal;
 RX MEDLINE=94105323; PubMed=8278527;
 RA Kunh A., Brunelle A., Shevell D., Chua N.-H.;
 RL "The CDNA sequence of two MADS box proteins in Petunia.";
 RL Plant Physiol. 102:1051-1052(1993).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. NECESSARY FOR THE NORMAL DEVELOPMENT OF
 CC PETALS. ABSENCE OF THE PMADS1 PROTEIN CAUSES TRANSFORMATION OF
 CC PETALS INTO SEALS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in petals and stamens,
 CC less in carpels and sepals.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR ENBL: X69946; CAA9567.1; --

DR PIR: S31693; S31693.
 DR HSS2; P11746; 1MMN.
 DR TRANSFAC; T01777; --
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADS-DOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Developmental protein.
 FT DOMAIN 3
 FT DOKAIN 93 165 MADS-box.
 SQ SEQUENCE 231 AA; 27039 MW; 76A5E0B3486B6F CRC64;
 Query Match 52.8%; Score 641.5; DB 1; Length 231;
 Best Local Similarity 55.6%; Pred. No. 4.8e-39;
 Matches 129; Conservative 36; Mismatches 52; Indels 15; Gaps 4;
 QY 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSILMLSTNKNMHEIYSP 60
 DB 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSILMLSTNKNMHEIYSP 60
 QY 61 TTTTSMYDYQKTMGIDLMRTHEESMKDTLWKLEINNKLRREIRQLGHDINGLSFDE 120
 DB 61 TTTTSMYDYQKTMGIDLMRTHEESMKDTLWKLEINNKLRREIRQLGHDINGLSFDE 120
 QY 121 LASIDDEMGSLLDAIRQKRVHVTQCTETTKKKYKNLEQRGMMLHGYPQEAAGEDPOY 180
 DB 121 LEBLMEVNDLSLKIRERKRVISNOIDTSKKKRVNVEIHRNLV--LEFDRARDDPAF 176
 QY 181 GYEDNEGYESALASNGANNLTFFHL--HHNLIHGGSSIGSSIT 224
 DB 177 GLVNEGDYNSVLGFPNGGRITALLRLQPNHGHQNHHLHSGG--GSDIT 225
 RESULT 3
 ID AP3_ARATH STANDARD; PRT; 232 AA.
 AC P35632; Q39003; Q81879; Q9S703; Q9S014; Q9S015; Q9S016; Q9S017;
 AC Q9S018; Q9S019; Q9S020; Q9S021; Q9S022; Q9S023; Q9S024;
 DT 01-JUN-1994 (Rel. 28, Created)
 DT 01-JUN-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein AP3AL3.
 GN AP3 OR AT3G54340 OR T12E18.30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eustoidia II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal;
 RX MEDLINE=92154682; PubMed=1346756;
 RA Jack T., Brockman L.L., Meyerowitz E.M.;
 RL "The homeotic gene AP3AL3 of Arabidopsis thaliana encodes a MADS
 RL box and is expressed in petals and stamens.";
 RL Cell 68:683-697(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=95035018; PubMed=7948893;
 RA Okamoto H., Yano A., Shiraiishi H., Okada K., Shimura Y.;
 RL "Genetic complementation of a floral homeotic mutation, ap3al3,
 RL with an Arabidopsis thaliana gene homologous to DEFICIENS of
 RL Antirrhinum majus.";
 RL Plant Mol. Biol. 26:465-472(1994).
 RN [3]
 RP SEQUENCE FROM N.A. AND VARIANTS.
 RC STRAIN=cv. Bia-1, cv. Bretagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,

RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,
RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,
RC cv. Li-3, cv. Li-8, and cv. Liese;
RX MEDLINE=99126449; PubMed=9927474;
RA Putuganan M.D., Suddith J.I.,
RT "Molecular population genetics of floral homeotic loci: departures
RT from the equilibrium-neutral model at the *APETALA3* and *PISTILLATA*
RT genes of *Arabidopsis thaliana*,"
RL Genetics 151:839-848(1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=1130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unsel'd M.,
RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaler B.,
RA Delany M., Boutry M., Grievell L.A., Maché R., Pulgomech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Queirer P.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wuebbach E., Drzonek H., Erile H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelico M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharte M., Schoen O., Bagnies M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottensmeyer B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masny D.,
RA de Haan M., Maiese A., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Agirretxu A., Flores M., Lignori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mees H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uteback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maltz R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltschew J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Matsumae A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant *Arabidopsis*
RT *thaliana*,"
RL Nature 408:820-822(2000).
[5]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.,
RT "Full-length cDNA from *Arabidopsis thaliana*,"
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954650; PubMed=14593172;
RA Yamada K., Lin J., Dale J.M., Chen H., Shim P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Mizunda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anstey Y.,
RA Akawa T., Banth J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao O., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ienida J., Jiang P.X., Jones T., Kawai J.,
RA Kamaya A., Meyers C., Nakajima M., Narukawa M., Seki M., Sakurai T.,
RA Satou M., Tame R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
RT "Empirical analysis of transcriptional activity in the *Arabidopsis*
RT genome,"
RL Science 302:842-846(2003).
[7]
RP SEQUENCE OF 36-128 FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99311297; PubMed=10382288;
RA Brunel D., Froger N., Pelletier G.,
RT "Development of amplified consensus genetic markers (ACGM) in *Brassica*

RT napus from *Arabidopsis thaliana* sequences of known biological
RT function,"
RL Genome 42:387-402(1999).
[8]
RP FUNCTION.
RX MEDLINE=96152196; PubMed=8565821;
RA Krizek B.A., Meyerowitz E.M.,
RT "The *Arabidopsis* homeotic genes *APETALA3* and *PISTILLATA* are sufficient
RT to provide the B class organ identity function,"
RL Development 122:11-22(1996).
[9]
RP CHARACTERIZATION.
RX MEDLINE=96209811; PubMed=8643482;
RA Riechmann J.L., Krizek B.A., Meyerowitz E.M.,
RT "Dimerization specificity of *Arabidopsis* MADS domain homeotic proteins
RT *APETALA1*, *APETALA3*, *PISTILLATA*, and *AGAMOUS*,"
RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
[10]
RP GENETIC REGULATION.
RX MEDLINE=21178805; PubMed=11283333;
RA Ng M., Yanofsky M.F.,
RT "Activation of the *Arabidopsis* B class homeotic genes by *APETALA1*,"
RL Plant Cell 13:739-753(2001).
[11]
RP CHARACTERIZATION.
RX MEDLINE=21074934; PubMed=11206550;
RA Homma T., Goto K.,
RT "Complexes of MADS-box proteins are sufficient to convert leaves into
RT floral organs,"
RL Nature 405:525-529(2001).
-1- FUNCTION: Probable transcription factor involved in the genetic
CC control of flower development. Is required for normal development
CC of petals and stamens in the wild-type flower. Forms an
CC heterodimer with *PISTILLATA* that is required for autoregulation of
CC both *AP3* and *PI* genes. *AP3/PI* heterodimer interacts with *APETALA1*
CC or *SEPALLATA3* to form a ternary complex that could be responsible
CC for the regulation of the genes involved in the flower
CC development.
-1- SUBUNIT: Forms a heterodimer with *PISTILLATA*, capable of binding
CC to CARG-box sequences. *AP3/PI* heterodimer binds *AP1* or *SEP3* to
CC form complexes.
-1- SUBCELLULAR LOCATION: Nuclear.
CC
-1- TISSUE SPECIFICITY: Expressed in petals and stamens.
CC
-1- INDUCTION: Positively regulated by the meristem identity proteins
CC *APETALA1* and *LEAFY* with the cooperation of UFO.
CC
-1- MISCELLANEOUS: Mutations in *AP3* cause transformation of petals
CC into sepals and stamens into carpels.
CC
-1- SIMILARITY: Contains 1 MADS-box domain.
CC
-1- SIMILARITY: Contains 1 MADS-box domain.
CC

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CC or send an email to license@isb-sib.ch).

DR EMBL; M6357; AAA32740.1; -;
DR EMBL; D21125; BAA04665.1; -;
DR EMBL; AF115798; AAD51887.1; -;
DR EMBL; AF115799; AAD51888.1; -;
DR EMBL; AF115800; AAD51889.1; -;
DR EMBL; AF115801; AAD51890.1; -;
DR EMBL; AF115802; AAD51891.1; -;
DR EMBL; AF115803; AAD51892.1; -;
DR EMBL; AF115804; AAD51893.1; -;
DR EMBL; AF115805; AAD51894.1; -;
DR EMBL; AF115806; AAD51895.1; -;
DR EMBL; AF115807; AAD51896.1; -;
DR EMBL; AF115808; AAD51897.1; -;
DR EMBL; AF115809; AAD51898.1; -;
DR EMBL; AF115810; AAD51899.1; -;

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CC -----

DR EMBL; X69947; CAA9568.1; -.
DR PIR; S31707; S31707.
DR HSSP; P11746; IKNM.
DR TRANSFAC; T03134; -.
DR InterPro; IPR002487; TF_Xbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRP-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW Developmental protein.
KW DOMAIN
FT DOMAIN 3 58 MADS-box.
FT DOMAIN 93 165 K-BOX.
SQ SEQUENCE 212 AA; 24785 MW; FCB10C16D52E4210 CRC64;

Query Match 31.7%; Score 385; DB 1; Length 212;
Best Local Similarity 37.9%; Pred. No. 8,3e-21;
Matches 85; Conservative 40; Mismatches 73; Indels 26; Gaps 4;

QY 1 MARGKIEIKLIENTQNTROYVYSKRNGIFKKAQELTVLDAKVSILMLSTNKKHEVTSY 60
DB 1 MGRGKIEIKRIENSSNRQVYTSKRNGIIRKAKETIVLCAKVSIIIRGNSGKMEYCS 60
QY 61 TTTTKSMVDVQKTMGIDLPRTFHESSMDTLWKLEINNKLRREIRGLTGHDLNLSFDE 120
DB 61 STLPEDMDGYOKSGRRLMDAKENLSNEIDRIKENDNQVQRHLKGEINLSLNHKE 120
QY 121 LASLDDEMOSSIDAIRQRKYHVIKTQTTTKRYKNLSEFORGNMLHGFDEAAGE--- 176
DB 121 LMTVEEGLTNGSSISAKOSELR---MVRNDDITLSEHKQLQYALHQEKVAMGGM 176
QY 177 ---DPQYGYEDNEGDYESALSLNSGANNLLYTFHLH---HPLH 213
DB 177 RMIEVYHQRDRDREYEQ-----MPPALRVQPMQPMYH 209

RESULT 6
M13_GNEG1 STANDARD; PRT; 237 AA.
ID M13_GNEG1
AC Q9XGU4.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE MADS box protein GCM13.
GN GCM13.
OS Gnetum gnetum (Bago).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
OC NCBI_TaxID=3382;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99307411; PubMed=10377416.
RA Winter K.-U., Becker A., Muenster T., Kim J.T., Saedler H.,
RA Theissen G.;
RT "MADS-box genes reveal that gnetophytes are more closely related to
RT conifers than to flowering plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:7342-7347(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=21851234; PubMed=11862488;
RA Becker A., Kaufmann K., Freilaidenhoven A., Vincent C., Li M.-A.,
RA Saedler H., Theissen G.;

"A novel MADS-box gene subfamily with sistergroup relationship to class B floral homeotic genes."

Mo. Genet. Genomes 266:942-950(2002).

CC -1- FUNCTION: Probable transcription factor.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- TISSUE SPECIFICITY: Expression specific for female reproductive structures: strong at the adaxial base of the cupules, where ovules will later develop, then in the outermost cell layer of the nucellus, in the inner envelope, and in the inner half of the middle envelope at late stage of ovule development.

CC -1- SIMILARITY: Contains 1 K-box dimerization domain.

CC -1- SIMILARITY: Contains 1 MADS-box domain.

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CC CC

DR EMBL; AJ132219; CAB44459.1; -.

DR HSPB; P11746; INNM. TF_KOXX.

DR InterPro; IPR002487; TF_KOXX.

DR InterPro; IPR002100; TF_MADSbox.

DR Pfam; PF01486; K-box; 1.

DR Pfam; PF00319; SRP-TE; 1.

DR PRINTS; PR00404; MADSDOMAIN.

DR SMART; SM00432; MADS; 1.

DR PROSITE; PS00350; MADS_BOX_1; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.

DR Trnscript; Transcription regulation; DNA-binding; Nuclear protein.

DR KX DOMAIN 1 61 MADS-box.

FT DOMAIN 69 170 K-BOX.

SO SEQUENCE 237 AA; 26943 MW; 5C65191A51D08691 CRC64;

Query Match 28.8%; Score 350.5; DB 1; Length 237;
Best Local Similarity 36.8%; Pred. No. 2,7e-18;
Matches 82; Conservative 45; Mismatches 85; Indels 11; Gaps 3;

Qy 1 MARGKIKIKIENQTRQVYYSKRRNIGFPKAOELTYLCAKAVSLMTSNTNKHETISP 60
Db 1 MGRKIKIKIKIENTTNKQVTFPSRRGGLKKAHSLVLCDEHGLITFSSGKLFETSSA 60

Qy 61 TTTTSMYDDYQKTMGIDLWRTHESMKOTLMKKEINNKLRREIRQLGHDLGSLFDE 120
Db 61 SSSMKIKIERYQKVGARITEYDNOHLCEMTBKNENKELQTVIRRMWGEDLTSLMTTE 120

Qy 121 LASLDDMOSLDAIRKRYHVIKIQETITKKYKYNLEGRGNMLHGYFPOEAAAGDPD- 179
Db 121 LHHGQQLLESASSRVRKRYQLMLQCELENTFRKRILEDQNSHLCLLAEGQAAVEGVQZ 180

Qy 180 ----YGYEDNEGDYESALALNSG----ANNLIYTFHLH--HPNL 212
Db 181 PLLEFGVFCPPBDKMTAAANAGGLHLGHLPAPRLQPTQNL 223

RESULT 7
ID GLOB ANTWA STANDARD; PRF; 215 AA.
AC 003378;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE GLOB homeotic protein GLOBOSA.
GN GLO.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Antirrhinaceae; Antirrhineae; Antirrhinum; Antirrhinum.
CK NCBI_TaxID=4151;
LN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=93099842; PubMed=1361166;
 RA Treiber W., Ramirez L., Motte P., Hue I., Huijser P., Loening M.-E.,
 RA Siedler H., Sommer H., Schwartz-Sommer Z.,
 RT "GLOBOSA: a homeotic gene which interacts with DEFICIENS in the
 RL control of Arabidopsis floral organogenesis.";
 CC EMO J. 11:4693-4704(1992).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: MUTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS
 CC INTO SEPAL AND STAMINA INTO CARPELS.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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 CC -----
 CC EMBL: X68831; CAA48725.1; -
 CC PIR: S28062; S28062.
 CC HSSP: P11746; 1MMN.
 CC TRANSFAC: T01778; -
 CC InterPro: IPR002487; TF_Kbox.
 CC InterPro: IPR002100; TF_MADSbox.
 CC Pfam: PF00486; K-box; 1.
 CC Pfam: PF00319; SRP-TF; 1.
 CC PRINTS: PR00404; MADSDOMAIN.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_2; 1.
 CC PROSITE: PS50066; MADS_BOX_1; 1.
 CC Transcription regulation; DNA-binding; Activator; Nuclear protein;
 CC Developmental protein.
 CC DOMAIN 3 MADS-box.
 CC FT DOMAIN 3 57 K-BOX.
 CC SEQUENCE 215 AA; 25363 MW; 0DE2A3E37815B7E4 CRC64;
 SQ
 Query Match 28.6%; Score 347.5; DB 1; Length 215;
 Best Local Similarity 34.1%; Pred. No. 4e-18; Indels 29; Gaps 5;
 Matches 77; Conservative 49; Mismatches 71;
 QY 1 MARGKIKELIENQTNQVYTSKRNGIFPKAQLVLCDAKYSILMSTNKHIEYISP 60
 DB 1 MGRKIKELIENSSNQVYTSKRNGIMKAKESIVLCDAKYSVILFASSGKMHFESP 60
 QY 61 TTTTSMYDDYQKTMGIDLRTHESKMDTLKKEINNKLRREIRQLGHDNLGSLFDE 120
 DB 61 STLVLDMDYHKLSGKRLWDPKHEHLDNEINVKKENDSMQELRLKGEEDITTLNHYE 120
 QY 121 LASLDDEMOSSLDLRKRYKTVIK-----TQETTKKKYKNLEQRGNMLHGY 168
 DB 121 LMTLEDALDNGLTSLRKQKMEFYAMRKKNHMYEENQSIQFLRQMDLPMNDVNM--- 177
 QY 169 FDOEAGEDEPOYGEDNEGDYESALALSGANNLYTFHLH--HPTL 212
 DB 178 -ESQAYVD---HHHQNIADYEAKMP-----FAFRVQPMCPNL 211
 RESULT 8
 GLOB_T0BAC STANDARD; PRT; 209 AA.
 AC Q03416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein GLOBOSA.
 GN GLO.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI Taxid=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV. SR1; Tissue=Flower;
 RX MEDLINE=93288002; PubMed=8099711;
 RA Hansen G., Estruch J.J., Sommer H., Spena A.,
 RT "NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of
 RL Arabidopsis majus: cDNA sequence and expression pattern.";
 CC Mol. Gen. Genet. 239:310-312(1993).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN FLORAL ORGANS AND, WITHIN
 CC THE FLOWER, EXPRESSION IS RESTRICTED TO PETALS AND STAMENS.
 CC -1- MISCELLANEOUS: MUTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS
 CC INTO SEPAL AND STAMINA INTO CARPELS.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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 CC -----
 CC EMBL: X67959; CAA48142.1; -
 CC PIR: S35226; S35226.
 CC HSSP: P11746; 1MMN.
 CC TRANSFAC: T01779; -
 CC InterPro: IPR002487; TF_Kbox.
 CC InterPro: IPR002100; TF_MADSbox.
 CC Pfam: PF00486; K-box; 1.
 CC Pfam: PF00319; SRP-TF; 1.
 CC PRINTS: PR00404; MADSDOMAIN.
 CC SMART: SM00432; MADS; 1.
 CC PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.
 CC Transcription regulation; DNA-binding; Activator; Nuclear protein;
 CC Developmental protein.
 CC DOMAIN 3 MADS-box.
 CC FT DOMAIN 3 57 K-BOX.
 CC SEQUENCE 209 AA; 24691 MW; 5661F9C1640E1A47 CRC64;
 SQ
 Query Match 28.0%; Score 340.5; DB 1; Length 209;
 Best Local Similarity 34.7%; Pred. No. 1.2e-17; Indels 21; Gaps 5;
 Matches 76; Conservative 49; Mismatches 73;
 QY 1 MARGKIKELIENQTNQVYTSKRNGIFPKAQLVLCDAKYSILMSTNKHIEYISP 60
 DB 1 MGRKIKELIENSSNQVYTSKRNGILKAKESIVLCDAKYSVILFASSGKMHFESP 59
 QY 61 TTTTSMYDDYQKTMGIDLRTHESKMDTLKKEINNKLRREIRQLGHDNLGSLFDE 120
 DB 61 TSVLVDLDYHKLGRRLWDKHEHLDNEINVKKENDSMQELRLKGEEDITSLNHYE 118
 QY 121 LASLDDEMOSSLDLRKRYKTVIK-----TQETTKKKYKNLEQRGNMLHGY 168
 DB 121 LMTLEDALDNGLTSLRKQKMEFYAMRKKNHMYEENQSIQFLRQMDLPMNDVNM--- 174
 QY 181 G-----YEDNEGDYESALALSGANNLYTFHLH--HPTL 212
 DB 175 GEIGEVFHRENEYQTMP-----FAFRVQPMCPNL 205
 RESULT 9
 M17_MAIZE STANDARD; PRT; 259 AA.
 AC Q8VMM8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein ZMM17.
 GN M17.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_Taxid=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. T232; TISSUE=flower;
 RX MEDLINE=21851234; Pubmed=11862488;
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,
 RA Saedler H., Theissen G., Freialdenhoven A., Vincent C., Li M.-A.,
 RA "A novel MADS-box gene subfamily with sistergroup relationship to
 RT class B floral homeotic genes.";
 RL Mol. Genet. Genomics 266:942-950 (2002).
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Strong expression in female inflorescences
 CC (ears), but also weak expression in male inflorescences (tassels).
 CC At early stages of the development of the female spikelet,
 CC expressed in all organ primordia but later restricted to the ovule
 CC and the developing silk. At very late stages of development,
 CC expression becomes restricted to parts of the silk.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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 CC -----
 CC DR EMBL; AJ271208; CAC81053.1; -
 CC DR InterPro; IPR002487; TF_Kbox.
 CC DR InterPro; IPR002100; TF_MADSbox.
 CC DR Pfam; PF01486; K-box; 1.
 CC DR Pfam; PF00319; SRF-TF; 1.
 CC DR PRINTS; PR00404; MADSBOX.M.
 CC DR SMART; SM00432; MADS; 1.
 CC DR PROSITE; PS00350; MADS_BOX_1; 1.
 CC DR PROSITE; PS00066; MADS_BOX_2; 1.
 CC FT Transcription regulation; DNA-binding; Nuclear protein.
 CC FT DOMAIN 1 61 MADS-box.
 CC FT DOMAIN 69 171 K-Box.
 CC FT SEQUENCE 259 AA; 29001 MW; B94E7F1D9420D44 CRC64;
 SQ
 Query Match 27.3%; Score 332; DB 1; Length 259;
 Best Local Similarity 33.0%; Pred. No. 6.3e-17;
 Matches 87; Conservative 46; Mismatches 93; Indels 38; Gaps 9;

RESULT 10
 ID PIST ARATH STANDARD; PRT; 208 AA.
 AC P48007; Q9S007; Q9S008; Q9S009; Q9S010; Q9S011; Q9S012; Q9S013;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein PISTILLATA (Transcription factor PI).
 GN PI OR AT5G20240 OR F5024.130.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=95047314; Pubmed=7958839;
 RA Goto K., Meyerowitz E.M.;
 RT "Function and regulation of the Arabidopsis floral homeotic gene
 RT PISTILLATA.";
 RL Genes Dev. 8:1548-1560 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=20233824; Pubmed=10769227;
 RA Honma T., Goto K.;
 RT "The Arabidopsis floral homeotic gene PISTILLATA is regulated by
 RT discrete cis-elements responsive to induction and maintenance
 RT signals.";
 RL Development 127:2021-2030 (2000).
 RN [3]
 RP SEQUENCE FROM N.A. AND VARIANTS.
 RC STRAIN=cv. Bla-1, cv. Bretagne, cv. Bs-1, cv. Bu-0, cv. Bu-2,
 RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cv1-0,
 RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,
 RC cv. Li-3, cv. Li-8, and cv. Lisse;
 RX MEDLINE=99126449; Pubmed=9927474;
 RA Purgscharan M.D., Sudhith J.I.;
 RT "Molecular population genetics of floral homeotic loci: departures
 RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
 RT genes of Arabidopsis thaliana.";
 RL Genetics 151:839-848 (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016721; Pubmed=1130714;
 RA Tabata S., Kaneo T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashina K.,
 RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
 RA Nakazaki N., Naruo K., Okumura S., Shino S., Takeuchi C., Wada T.,
 RA Matsumabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Haberman K., Murray J., Johnson D., Kohling T., Nelson J.,
 RA Soneking T., Pepin K., Spleth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney C., Dante M.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamer E., Latreille P.,
 RA Leonard S., Meyer K., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
 RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,
 RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
 RA Martensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volckert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
 RA Ertan K.-D., Terry N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Glynnoprez B., Zimmermann W.,
 RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirke W., Moolman P., Klein lankhorst R.,
 RA Weitzneger T., Bothe G., Rose W., Hauf J., Betzelser S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarroel R., Gelen J., Ardiles W.,
 RA Bente O., Lemcke K., Kolesov G., Mayer K.F.X., Rüd S., Schöot H.,
 RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.;

RT mutant petunia flowers.",
 RL Plant Cell 4:983-993(1992).
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: PETAL.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, M91190; AAA33731.1; -.
 DR PIR, J01689; J01689.
 DR HSP, F11746; ILMN.
 DR TRANSFAC; T03092; -.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 KW DOMAIN 3 57 MADS-box.
 FT DOMAIN 91 163 K-BOX.
 SQ SEQUENCE 210 AA; 24647 MW; B2D3718BE6A157C8E CRC64;
 Query Match 26.8%; Score 326; DB 1; Length 210;
 Best Local Similarity 40.9%; Pred. No. 1.3e-16;
 Matches 67; Conservative 41; Mismatches 50; Indels 6; Gaps 2;
 QY 1 MARGKIEKLTENQNNROVTVSKRNGIFKRAQELTVCDKAVSLMSTNNKHEVYSP 60
 DB 1 MGRGKIEKRLIENSNRQVTVSKRNGILKRAKESVLCDAVSIVLPASSGKHEFES- 59
 QY 61 TTTKSMVDVYQKTMGIDLMRTHEESMDKTLMKLEINNNKRLREIQRGLGDLNGLSFDE 120
 DB 60 -TSIVDILIDQYHKLGRRLDLAKHNLNENIKYKKDNNQIELRHKGEDISLNHRE 118
 QY 121 LASLDDMOSSLDARQKRTAVIKQTQETTTKKKVKNLFGRRGNM 164
 DB 119 LMLIEDALENGLTSIRNKQNEVLRW---RKKTQSMEEBDDQL 158
 RESULT 12
 ID TT16-ARATH STANDARD; PRT; 252 AA.
 AC Q8RYD9; Q8RFM4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE TRANSPARENT TESTA 16 protein (Arabidopsis BISISTER MADS box protein).
 GN TT16 OR ABS OR AT5G23260 OR MD15.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustersids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A. (TOROBN 1).
 RC STRAIN=cv. Columbia; TISSUE=green siliques;
 RX MEDLINE=21951234; PubMed=11862488;
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,
 RA Saedler H., Theissen G.,
 RT "A novel MADS-box gene subfamily with sistergroup relationship to
 RT class B floral homeotic genes";
 RL Mol. Genet. Genomics 266:942-950(2002).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asanizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned P1 clones";
 RL DNA Res. 4:401-414(1997).
 RN [3]
 RP CHARACTERIZATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=2226185; PubMed=12368498;
 RA Nesi N., Debeaujon I., Jond C., Stewart A.J., Jenkins G.I.,
 RA Caboche M., Lepointec L.;
 RT "The TRANSPARENT TESTA16 locus encodes the ARABIDOPSIS BISISTER MADS
 RT domain protein and is required for proper development and
 RT pigmentation of the seed coat";
 RL Plant Cell 14:2463-2479(2002).
 CC -1- FUNCTION: Transcription factor involved in the developmental
 CC regulation of the endodermium and in the accumulation of
 CC proanthocyanidins (PAS) or condensed tannins which give the seed
 CC its brown pigmentation after oxidation. Necessary for the normal
 CC activation of the BANYUS promoter in the endodermium body.
 CC -1- PATHWAY: Flavonoid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8RYD-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8RYD-2; Sequence=VSP_006257;
 CC -1- TISSUE SPECIFICITY: Expressed in buds, flowers and immature seeds,
 CC but not in roots, stems, leaves, seedlings or siliques valves.
 CC Expression in seed coat is confined to the endodermium layer.
 CC -1- DEVELOPMENTAL STAGE: Expressed during seed development.
 CC -1- MISCELLANEOUS: The two isoforms were always coexpressed in the
 CC tissues investigated. The pigmentation of the chalazal-micropyle
 CC region is not under the control of ABS, as opposed to the
 CC pigmentation of the seed body.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
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 CC -----
 DR EMBL, AJ318098; CAC8564.1; -.
 DR EMBL, AB007648; BAB1181.1; ALT_SEQ.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 KW Flavonoid biosynthesis; Transcription; Transcription regulation;
 KW DNA-binding; Alternative splicing; Nuclear protein; Coiled coil.
 FT DOMAIN 1 61 MADS-box.
 FT DOMAIN 73 172 K-BOX.
 FT DOMAIN 121 174 COILED COIL (POTENTIAL).
 FT DOMAIN 180 222 GIN-RICH.
 FT VARSPLIC 142 146 Missing (in isoform 2).
 FT SEQUENCE 252 AA; 29697 MW; 2C4ECB9D9DCIDEA8 CRC64;
 /FTID=VSP_006257.

DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 1 61 MADS-box.
 FT DOMAIN 74 177 K-BOX.
 SQ SEQUENCE 247 AA; 29052 MW; 7BEEF2BC7C504371 CRC64;
 Query Match 24.4%; Score 297.5; DB 1; Length 247;
 Best Local Similarity 37.9%; Pred. No. 1.7e-14;
 Matches 66; Conservative 35; Mismatches 64; Indels 9; Gaps 2;
 Oy 1 MARGKIEIKLIENTQNRQVTSKRRNGIFKKAQELTVLCAKVSILMLSNTKMHEYISP 60
 1 MGRGKIEIKLIENTSRQVTSKRRSGILMKTHLSVLCDAQILIVFTSGKLTCTP 60
 Db 1 TTTTSMYDDYQXTWGI-----DLWRTHEESKDTLWKLEINNKLRREIRQLGHD 112
 Oy 61 PFSMKQIIDRYVYKAKGILPEMENRAGPHADNDQVYKE-LTRMKETTLNLQNLQRYKGD 119
 Db 113 LNSGSPDELASLDDEMSSLDAIRORXKHYVTKTQETTKKKVKYLQORGNMLH 166
 120 LSTVRFELTELEKLDQSLMKVRKRLKELHGEQENLKRTFMLEKENQEMTH 173
 RESULT 15
 AG14 ARATH STANDARD; PRT; 221 AA.
 ID AG14 ARATH Q38838; Q9T056;
 AC 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Agamox-like MADS box protein AG14.
 GN AG14 OR AT4G11880 OR T26M18.90.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids 1; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RX MEDLINE=20083488; PubMed=10617198;
 RP STRAIN=cv. Columbia;
 RC Mayr K.F.X., Scheller C., Wandura R., Murphy G., Volckaert G.,
 Pohl T., Duesterhoef A., Stiekema W., Entlan K.-D., Terryn N.,
 Harris B., Ansoorge W., Brandt P., Grievell L.A., Rieger M.,
 Weichselgartner M., de Simone V., Obermayer B., Macho R., Weiler M.,
 Kreis M., Deiseny M., Pildomenech P., Watson M., Schmidheini T.,
 Reichert B., Portetle D., Perez-Alonso M., Boutry M., Bancroft I.,
 Vos P., Hobeisel J., Zimmermann W., Wedler H., Ridley P.,
 Langham S.-A., McCullagh B., Biham L., Roben J.,
 Van der Schueren J., Grymptre B., Chuang Y.-D., Vandenbusche F.,
 Bizeken M., Weltjens I., Voet R., Bastiaens I., Aert R., Defoor E.,
 Weltzenerger T., Bohe G., Rameberger U., Hilbert H., Braun M.,
 Holzner E., Brandt A., Peters S., van Staveren M., Dikse W.,
 Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetser P.,
 Bernier S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 de Keyser A., Buysmaert C., Gielen J., Villarroel R., De Clercq R.,
 Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
 Clark L., Doggett J., Hall S., Kay M., Leonard N., Molay K., Mayes R.,
 Perrett A., Rajandream M., Lyne M., Benes V., Rechmann S.,
 Borova D., Bloeker H., Scharfe M., Grimm M., Loehart T.-H.,
 Dore S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 Gabel C., Fuchs M., Fatmann B., Grandetath K., Damer D., Herl A.,
 Neumann S., Angillon A., Vitale D., Liqiori R., Piravandi E.,
 Maeser O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 Schnabl S., Hiller R., Berger C., Montfort A., Casacuberta E.,
 Ghibons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
 Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Biele C.,
 Frithman D., Haase D., Lemcke K., Wewes H.-M., Stocker S.,
 Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 Parrell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Clout J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Splich J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Dron K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekier M., Matero A., Shah R.,
 RA Saby I.K., O'Shaughnessy A., Rodriguez W., Holtman J., Till S.,
 RA Grant S., Shochdy N., Haegawa A., Hamed A., Lodi M., Johnson A.,
 RA Chen B., Marra M.A., Martienssen R., McCombie W.R.,
 RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana."
 RT thaliana.402:769-777(1999).
 RU Nature 402:769-777(1999).
 RN [2]
 RP SEQUENCE OF 7-221 FROM N.A.
 RC STRAIN=cv. Landsberg erecta; TISSUE=Root;
 RX MEDLINE=96004530; PubMed=7549482;
 RA Rounleay S.D., Ditta G.S., Yanofsky M.F.;
 RT "Diverse roles for MADS box genes in Arabidopsis development."
 RU Plant Cell 7:1259-1269(1995).
 CC - FUNCTION: Probable transcription factor.
 CC - SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC - TISSUE SPECIFICITY: Preferentially expressed in roots.
 CC - SIMILARITY: Contains 1 K-box dimerization domain.
 CC - SIMILARITY: Contains 1 MADS-box domain.
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 CC -----
 CC EMBL; AL078606; CAB44326.1; -;
 CC EMBL; AL161532; CAB78231.1; -;
 CC EMBL; U20184; AAC49082.1; -;
 CC PIR; T09347; T09347.
 CC HSP; P11746; IANM.
 CC TRANSFAC; T03012; -;
 CC InterPro; IPR002487; TF_KBOX.
 CC InterPro; IPR002100; TF_MADSBOX.
 CC Pfam; PF01486; K-box; 1.
 CC Pfam; PF00319; SRP-TR; 1.
 CC PRINTS; PR00404; MADSBOXMAIN.
 CC SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS-box.
 FT DOMAIN 96 168 K-BOX.
 FT CONFLICT 103 103 H -> D (IN REF. 2).
 FT CONFLICT 187 188 ST -> TS (IN REF. 2).
 SQ SEQUENCE 221 AA; 25492 MW; E876DAEA049B125E CRC64;
 Query Match 24.4%; Score 296.5; DB 1; Length 221;
 Best Local Similarity 41.4%; Pred. No. 1.8e-14;
 Matches 67; Conservative 35; Mismatches 53; Indels 7; Gaps 3;
 Oy 1 MARGKIEIKLIENTQNRQVTSKRRNGIFKKAQELTVLCAKVSILMLSNTKMHEYISP 60
 1 MVRGKIEIKLIENTSRQVTSKRRSGILMKTHLSVLCDAQILIVFTSGKLTCTP 60
 Db 1 TTTTSMYDDYQXTWGI-----ESMKDTLWKLEINNKLRREIRQLGHD 115
 Oy 61 PFSMKQIIDRYVYKAKGILPEMENRAGPHADNDQVYKE-LTRMKETTLNLQNLQRYKGD 119
 Db 116 LNSGSPDELASLDDEMSSLDAIRORXKHYVTKTQETTKKKVKYLQORGNMLH 157
 119 LSTVRFELTELEKLDQSLMKVRKRLKELHGEQENLKRTFMLEKENQEMTH 160

Search completed: September 27, 2004, 09:25:46
Job time : 17.5705 secs

DR SMART; SM00432; MADS_1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 232 AA; 26898 MW; 7308DA605540F9C CRC64;

Query Match 98.9%; Score 1203; DB 10; Length 232;
 Best Local Similarity 99.1%; Pred. No. 5.8e-86;
 Matches 230; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARGIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPDAKYSILMTSNTNQHXYISP 60
 DB 1 MGRKIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPDAKYSILMTSNTNQHXYISP 60
 QY 61 TTTTSMYDDYQKTMGIDLMRTHEESKMDTLMKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 DB 61 TTTTSMYDDYQKTMGIDLMRTHEESKMDTLMKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 QY 121 LASLDDMOSSLDAIRQKHYVITQETTTKKYKYNLEORGNMLHGYPQDAAGDPQY 180
 DB 121 LASLDDMOSSLDAIRQKHYVITQETTTKKYKYNLEORGNMLHGYPQDAAGDPQY 180
 QY 181 GYEDNEGYSALALSNGANNTYTFHLHPNLHHGSSIGSSITTHLDRLA 232
 DB 181 GYEDNEGYSALALSNGANNTYTFHLHPNLHHGSSIGSSITTHLDRLA 232

RESULT 2

QBLSM8 PRELIMINARY; PRT; 237 AA.

ID QBLSM8
 AC QBLSM8
 DT 01-OCT-2002 (TREMREL. 22, Created)
 DT 01-OCT-2002 (TREMREL. 22, Last sequence update)
 DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
 DE MADS-box protein.
 GN MDM6.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 1; Rosales; Rosaceae; Maloideae; Malus.
 OC NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Indo; TISSUE=young floral parts;
 RA Matsumoto S., Ohtsubo T., Soejima Y.,
 RT "Cloning and sequencing of apple MADS-box genes 'MdPI', 'MDTM6', and
 RT 'MdMDS13'."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AB081093; BAB1907.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS_1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 237 AA; 27693 MW; 71A2B357202FCF20 CRC64;

Query Match 88.2%; Score 1072.5; DB 10; Length 237;
 Best Local Similarity 87.9%; Pred. No. 8.8e-76;
 Matches 211; Conservative 9; Mismatches 9; Indels 11; Gaps 3;
 QY 1 MARGIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPDAKYSILMTSNTNQHXYISP 60

DB 1 MGRKIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPDAKYSILMTSNTNQHXYISP 60
 QY 61 TTTTSMYDDYQKTMGIDLMRTHEESKMDTLMKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 DB 61 TTTTSMYDDYQKTMGIDLMRTHEESKMDTLMKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 QY 121 LASLDDMOSSLDAIRQKHYVITQETTTKKYKYNLEORGNMLHGYPQDAAGDPQY 180
 DB 121 LASLDDMOSSLDAIRQKHYVITQETTTKKYKYNLEORGNMLHGYPQDAAGDPQY 180
 QY 181 GYEDNEGYSALALSNGANNTYTFHLHPNLHHGSSIGSSITTHLDRLA 232
 DB 181 GYEDNEGYSALALSNGANNTYTFHLHPNLHHGSSIGSSITTHLDRLA 232

RESULT 3

ID Q93X10 PRELIMINARY; PRT; 261 AA.

AC Q93X10
 DT 01-DEC-2001 (TREMREL. 19, Created)
 DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
 DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
 DE MADS-box protein.
 GN MASAKO B3.
 OS Rosa rugosa (Rugosa rose).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 1; Rosales; Rosaceae; Rosoideae; Rosa.
 OC NCBI_TaxID=74645;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Young floral parts;
 RA Matsumoto S., Hirai S., Kishihara K.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Young floral parts;
 RA Kishihara K., Hirai S., Fukui H., Matsumoto S.;
 RT "Rose MADS-box genes 'MASAKO B' and B3' homologous to class B floral
 RT identity genes'".
 RL Plant Sci. 161:549-557(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AB055966; BAB3261.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS_1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 261 AA; 29777 MW; 6EBD1283977E05E CRC64;

Query Match 72.6%; Score 882.5; DB 10; Length 261;
 Best Local Similarity 66.2%; Pred. No. 6.5e-61;
 Matches 174; Conservative 24; Mismatches 32; Indels 33; Gaps 3;

QY 1 MARGIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPDAKYSILMTSNTNQHXYISP 60
 DB 1 MGRKIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPDAKYSILMTSNTNQHXYISP 60
 QY 61 TTTTSMYDDYQKTMGIDLMRTHEESKMDTLMKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 DB 61 TTTTSMYDDYQKTMGIDLMRTHEESKMDTLMKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 QY 121 LASLDDMOSSLDAIRQKHYVITQETTTKKYKYNLEORGNMLHGYPQDAAGDPQY 180

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Db 121 LQDLEMTSGSVQIRKDKYHVLKQATTTTKKYNLEERSNLMHG--GAPGNEBPQY 178
QY 181 GYEDNEGDYESALALNSGANNLYTF-----HLHPVLA----- 213
Db 179 GYVNEGDYESVALANGASNLTFPNRVHNNHLDHGGGSLVSTLTHLQNPVHGNHN 238
QY 214 ----HGSSLSGSSITLHDLRLA 232
Db 239 LENGHGSSLSITLHDLRLA 261

RESULT 4
09L1A1
ID 09L1A1 PRELIMINARY; PRT; 225 AA.
AC 09L1A1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE MADS box transcription factor TM6.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Petunia.
OC NCBI_TaxID=4102;
OX [1]
RN SEQUENCE FROM N.A.
RA Kramer E.M., Irish V.F.;
RT "Evolution of the petal and stamen developmental programs: Evidence
RT from comparative studies of the lower eudicots and basal
RT angiosperms."
RL Int. J. Plant Sci. 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF230704; AAF73933.1; -.
DR HSBP; P11746; IMNM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00319; SRF-TF; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 225 AA; 26047 MW; 765515B38AC4C5DD CRC64;

Query Match 59.3%; Score 721.5; DB 10; Length 225;
Best Local Similarity 60.7%; Pred. No. 1.9e-48;
Matches 142; Conservative 32; Mismatches 49; Indels 11; Gaps 4;

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RESULT 5
09ZS28
ID 09ZS28 PRELIMINARY; PRT; 226 AA.
AC 09ZS28;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE MADS-box protein, GDEF1.
OS Gerbera hybrida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteraceae; Multisididae; Gerbera.
OC NCBI_TaxID=18101;
OX [1]
RN SEQUENCE FROM N.A.
RA STRAIN=cy. Terra Regina;
RX MEDLINE=9168221; Pubmed=10069067;
RA Yu D., Kotilaenen M., Poelaeen E., Mehto M., Elomaa P.,
RA Helariutta Y., Albert V.A., Teeri T.H.;
RT "Organ identity genes and modified patterns of flower development in
RT Gerbera hybrida (Asteraceae)."
RL Plant J. 17:51-62(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AJ009724; CAA08802.1; -.
DR HSBP; P11746; IMNM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00319; SRF-TF; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 226 AA; 26556 MW; 1C2553CB5E4B997 CRC64;

Query Match 59.3%; Score 721.5; DB 10; Length 226;
Best Local Similarity 63.0%; Pred. No. 1.9e-48;
Matches 145; Conservative 24; Mismatches 50; Indels 11; Gaps 4;

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RA Boggio S., Valle E., Zabaleta E.J.;
 RT "MADS-box genes expressed during the tomato seed and fruit
 development."
 RL Submitted (NCV-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY038734; AAM3100.2; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADS_DOMAIN.
 DR SMART; SM00432; MADS_BOX_2; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 FT NON_TER
 SQ SEQUENCE 222 AA; 25843 MW; 67E61A125812A08 CRC64;

Query Match 56.8%; Score 690.5; DB 10; Length 222;
 Best Local Similarity 59.7%; Pred. No. 4,8e-46;
 Matches 138; Conservative 30; Mismatches 52; Indels 11; Gaps 4;

QY 4 GKEIKLIENTOTROVYTSKRRNGIFKKAQELTVLCAKVSILMLSTNKKHEYSPTT 63
 DB 1 GKEIKLIENTLNROVTFSSKRRNGIFKRRKELTVLCAKISILMLSTRKYHEYSPTT 60
 QY 64 TKSVDYDQKTMGIDLMRTHESMDTLMKKEINNKLRREIRQLGHDNGLSFDEIAS 123
 DB 61 TRKMDIQSALGVIVSIHERKQENLRKLEINNKLRREIRQLGHDNGLSFDEIAS 120
 QY 124 LDDEMOSSLDIAIRCKHYVITKTOTETTKKVKYKLEQRGNMLHGYFDOEAAGDPQY 183
 DB 121 LGENTESVAIREKHYVINKQDTCCKKARNLEQNGNLV---LDLEACEDPKYGV 177
 QY 184 DNEGDYSALALSGANNLYTFHLH--HPNTHGSSISGSSITTHDIRLA 232
 DB 178 ENEGHYSAVAFANGVHNLVAFRLQPLPHNLQNEG--GRGS-----RDRLRS 222

RESULT 9

Q84U28 PRELIMINARY; PRT; 238 AA.

AC Q84U28; DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE APETALA3

OS Populus tomentosa.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Eustoides I; Malpighiales; Salicaceae; Salicaceae; Populus.

NCBI_TaxID=118781;

11

SEQUENCE FROM N.A.

RA An X., Zhang Z., Li S.;
 RT "Molecular cloning of APETALA3 (AP3) homologous gene from male poplar
 (Populus tomentosa Car.)."

RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY210488; AAO49713.1; -

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR002487; TF_Kbox.

DR InterPro; IPR002100; TF_MADSbox.

DR Pfam; PF01486; K-box; 1.

DR Pfam; PF00319; SRF-TF; 1.

DR PRINTS; PR00404; MADS_DOMAIN.

DR SMART; SM00432; MADS_BOX_2; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.
 SQ SEQUENCE 238 AA; 27207 MW; 20EBA028350A4FE7 CRC64;

Query Match 56.1%; Score 682; DB 10; Length 238;

Best Local Similarity 58.5%; Pred. No. 2.4e-45;
 Matches 144; Conservative 28; Mismatches 50; Indels 24; Gaps 4;

QY 1 MARGKEIKLIENTOTROVYTSKRRNGIFKKAQELTVLCAKVSILMLSTNKKHEYSPTT 60
 DB 1 MARGKEIKLIENTPRTQVYTSKRRNGIFKKAQELTVLCAKVSILMLSTNKKHEYSPTT 60
 QY 61 TTTTSSVDDYDQKTMGIDLMRTHESMDTLMKKEINNKLRREIRQLGHDNGLSFDE 120
 DB 61 STSKKIVDQYQNTLIGIDLMGTOYERKQENLRKLEINNKLRREIRQLGHDNGLSFDE 120
 QY 121 LADDEMOSSLDIAIRCKHYVITKTOTETTKKVKYKLEQRGNMLHGYFDOEAAGDPQY 180
 DB 121 LRGLBQMTBALGVGRKHYVITKTOTETTKKVKYKLEQRGNMLHGYFDOEAAGDPQY 177
 QY 181 GYEDNE-----GDYESALALSGANNLYTFHLHHPNTHGSSISGSSITTHL----- 226
 DB 178 GLVDNEAAVALVDGASDNEAAVALADGASNLVAILRHGHNHHPN-----LHLEDGPG 231
 QY 227 HDLRL 231
 DB 232 AHELR 237

RESULT 10

Q9LLA2 PRELIMINARY; PRT; 201 AA.

AC Q9LLA2; DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE MADS box transcription factor TW6 (Fragment).

OS Hydrangea macrophylla.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Cornales; Hydrangeaceae; Hydrangea.

NCBI_TaxID=23110;

11

SEQUENCE FROM N.A.

RA Kramer E.M., Irish V.F.;
 RT "Evolution of the petal and stamen developmental programs: Evidence
 from comparative studies of the lower eudicots and basal

RT angiosperms."

RL Int. J. Plant Sci. 0:0-0(2000).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION

FACTORS.

DR EMBL; AF230703; AAF73932.1; -

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR002487; TF_Kbox.

DR InterPro; IPR002100; TF_MADSbox.

DR Pfam; PF01486; K-box; 1.

DR Pfam; PF00319; SRF-TF; 1.

DR SMART; SM00432; MADS_BOX_2; 1.

KM DNA-binding; Nuclear protein; Transcription; Transcription regulation.

FT NON_TER
 SQ SEQUENCE 201 AA; 23226 MW; 66928A89200A042 CRC64;

Query Match 54.2%; Score 659; DB 10; Length 201;
 Best Local Similarity 62.2%; Pred. No. 1.2e-43;

Matches 130; Conservative 25; Mismatches 44; Indels 10; Gaps 3;

QY 26 NGIFKKAQELTVLCAKVSILMLSTNKKHEYSPTTTSKVDYDQKTMGIDLMRTHES 85
 DB 1 NGIFKKAQELTVLCAKVSILMLSTNKKHEYSPTTTSKVDYDQKTMGIDLMRTHES 85
 QY 86 SMKDTLMKLEINNKLRREIRQLGHDNGLSFDEIASLDDEMOSSLDIAIRCKHYVIT 145
 DB 61 RMQEHRLKLEAVNKLRRREIRQLGHDNGLSFDEIASLDDEMOSSLDIAIRCKHYVIT 120

Qy 146 QTEETKKKKKXVLEORGNMLHGYPDEAGSDPOGYEDNEGDEYSAALNSGANNLYTF 205
 Db 121 QTEETCKKKKXVLEORGNMLHGYPDEAGSDPOGYEDNEGDEYSAALNSGANNLYTF 177
 Qy 206 HLH--HFNLRHGSSSLGSSITTHDLRLA 232
 Db 178 GLQPSHPLHNGGGGGS-----HDLRLA 201

RESULT 11

ID Q40513 PRELIMINARY; PRT; 227 AA.
 AC Q40513;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE MADS-box protein.
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 CC Lamiales; Solanales; Solanaceae; Nicotiana.
 CC NCBI_Taxid=4097;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA MEDLINE=97046712; PubMed=8893543;
 RA Davies, D; Rosa, Eneva, Saedler, Sommer;
 RT "Alteration of tobacco floral organ identity by expression of
 combinations of Antirrhinum MADS-box genes."
 RL Plant J. 10:663-677(1996).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL: X96428; CAA65288.1; -.
 DR HSSP; P11746; IMMW.
 DR TRANSFAC; T03109; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 227 AA; 26401 MW; FEF88A9A2AD7FEC4 CRC64;

Query Match 52.5%; Score 638; DB 10; Length 227;
 Best Local Similarity 56.3%; Pred. No. 6.1e-42;
 Matches 129; Conservative 36; Mismatches 52; Indels 12; Gaps 5;

Qy 1 MARGKIEIKLIENQTNQVYTSKRNGIFKKAQELTVLCAKYSILMSNTNMGHEIYSP 60
 Db 1 MARGKIQIKLIENQTNQVYTSKRNGIFKKAQELTVLCAKYSILMSNTNMGHEIYSP 60
 Qy 61 TTTTKSMYDYOXTMGIDLMRTHEESKMDTLMLKEINNKLRRIROGLHDLNGLSFE 120
 Db 61 SVTTKQFLDYQKTVGIDLMNSHYEKQEQRLKLDVNRRLRRIHQRMGESLNDLNFQ 120
 Qy 121 LASIDDEMOSSLDAIRORXKXVIVKTQETTKKKKXVLEORGNMLHGYPDEAGSDPOY 180
 Db 121 LEELMENVDNLSKLIIRKXKXVIVGNQIDTYKKKXVLEORGNMLHGYPDEAGSDPOY 176
 Qy 181 GYEDNEGDEYSAALNSGANNLYTFHL--HFN--LHNGSSSLGSSIT 224
 Db 177 GLVEQSGDYNSVLGFPNGSPRIILRLQPMHQPMHHLHSG--GSDIT 222

RESULT 12

Q41417
 ID Q41417 PRELIMINARY; PRT; 228 AA.
 AC Q41417;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Deficiens analogue.
 GN DEF4.
 OS Solanum tuberosum (Potato).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 CC Lamiales; Solanales; Solanaceae; Solanum.
 CC NCBI_Taxid=4113;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA STRAIN=Granola; TISSUE=leaf;
 RA MEDLINE=94100991; PubMed=7903890;
 RA Garcia-Maroto F; Salami F; Rohde W;
 RT "Molecular cloning and expression patterns of three alleles of the
 Deficiens-homologous gene St-deficiens from Solanum tuberosum."
 RL Plant J. 4:771-780(1993).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL: X67511; CAA47846.1; -.
 DR PIR; T07066; T07066.
 DR HSSP; P11746; IMMW.
 DR TRANSFAC; T03179; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR PRINTS; PR00404; MADSOMAIN.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00319; SRP-TF; 1.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 228 AA; 26367 MW; 8568024C423BE93F CRC64;

Query Match 51.7%; Score 628.5; DB 10; Length 228;
 Best Local Similarity 54.1%; Pred. No. 3.4e-41;
 Matches 124; Conservative 40; Mismatches 54; Indels 11; Gaps 3;

Qy 1 MARGKIEIKLIENQTNQVYTSKRNGIFKKAQELTVLCAKYSILMSNTNMGHEIYSP 60
 Db 1 MARGKIQIKLIENQTNQVYTSKRNGIFKKAQELTVLCAKYSILMSNTNMGHEIYSP 60
 Qy 61 TTTTKSMYDYOXTMGIDLMRTHEESKMDTLMLKEINNKLRRIROGLHDLNGLSFE 120
 Db 61 SITTKQFLDYQKTVGIDLMNSHYEKQEQRLKLDVNRRLRRIHQRMGESLNDLNFQ 120
 Qy 121 LASIDDEMOSSLDAIRORXKXVIVKTQETTKKKKXVLEORGNMLHGYPDEAGSDPOY 180
 Db 121 LEELMENVDNLSKLIIRKXKXVIVGNQIDTYKKKXVLEORGNMLHGYPDEAGSDPOY 177
 Qy 181 GYEDNEGDEYSAALNSGANNLYTFHL--HFN--LHNGSSSLGSSIT 224
 Db 178 GLVEQSGDYNSVLGFPNGSPRIILRLQPMHNNHHHLHSG--GSDIT 223

RESULT 13

ID Q41477 PRELIMINARY; PRT; 228 AA.
 AC Q41477;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Deficiens analogue.

OS Solanum tuberosum (potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H81.1506/60; TISSUE=Flower;
 RX MEDLINE=94100991; PubMed=7903890;
 RA Garcia-Maroto F., Salami F., Ronde W.;
 RT Molecular cloning and expression patterns of three alleles of the
 RT Deficient-homologous gene St-deficiens from Solanum tuberosum.";
 RL Plant J. 4:771-780(1993).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; X67508; CAA47845.1; -.
 DR PIR; T07410; T07410.
 DR HSSP; P11746; INNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00065; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 228 AA; 26339 MW; DD4BE1D9AA3E4DF CRC64;
 Query Match 51.4%; Score 624.5; DB 10; Length 228;
 Best Local Similarity 53.7%; Pred. No. 6,9e-41;
 Matches 123; Conservative 41; Mismatches 54; Indels 11; Gaps 3;
 QY 1 MARGKIKIKIENQNRQVYSSRRNGIFPKKAQELTVLCAKAVSLIMLNTNKHETISP 60
 DB 1 MARGKIQKIKIENQNRQVYSSRRNGIFPKKANELTVLCAKAVSIWMSISGKIHETISP 60
 QY 61 TTTTSMVDYQKTMGIDLWRTHEESMDTLMKKEINNKLRREIRORLGHDLNGSPDE 120
 DB 61 SITNNLDPYQKTVGIDWTSYKMOELRKLADVNRNLRKEIRORWGSGLNDLNPQ 120
 QY 121 LASLDDEMOSSLDAIRORRYVITQTEETTKKVKVNLQRGNMLHGYFDOAAGDPQY 180
 DB 121 LEELEENVDNLSKLRERKVKVINGQIEYRKRVANVEIHRNLL--LEFDARQEDPYG 177
 QY 181 GYEDNEGDIYSALANSANNLYTHLH--HNNLHGGSSLSGSIT 224
 DB 178 GLVEQEGDYNVSLGPPTGGHLLALGLQPNNNHHHLLHSG--GSDIT 223
 RESULT 14
 Q40352 PRELIMINARY; PRT; 247 AA.
 AC Q40352;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE MADS-box protein.
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Node1;
 RX MEDLINE=95296292; PubMed=7777496;
 RA Heard J., Dunn K.;

RT "Symbiotic induction of a MADS-box gene during development of alfalfa
 RT root nodules.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5273-5277(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Node1;
 RA Dunn K.;
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; L41727; AAB48660.1; -.
 DR HSSP; P11746; INNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 247 AA; 28645 MW; B19EF55F7BAC89E7 CRC64;
 Query Match 51.3%; Score 623.5; DB 10; Length 247;
 Best Local Similarity 54.4%; Pred. No. 9,2e-41;
 Matches 123; Conservative 35; Mismatches 63; Indels 5; Gaps 2;
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 DB 1 MARGKIQKIKIENQNRQVYSSRRNGIFPKKANELTVLCAKAVSIWMSISGKIHETISP 60
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 DB 61 SASIKQFPDQYQTVGIDWTSYKMOELRKLADVNRNLRKEIRORWGSGLNDLNPQ 120
 QY 121 LASLDDEMOSSLDAIRORRYVITQTEETTKKVKVNLQRGNMLHGYFDOAAGDPQY 180
 DB 121 LRLLEDEMDELKALIRERKVKVINGQIDQKFFNERREVDNLLR--DLDAARDPRF 177
 QY 181 GYEDNEGDIYSALANSANNLYTHLH--HNNLHGGSSLSGSIT 224
 DB 178 EMDNNGEYYSVIGFNLGRFALSLQPTHPNNGASAAASDIT 223
 RESULT 15
 Q65141 PRELIMINARY; PRT; 228 AA.
 AC Q65141;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE APETALA3 homolog PpAP3-2.
 OS Papaver nudicaule.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Papaveraceae; Papaver.
 OX NCBI_TaxID=74823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278797; PubMed=9611190;
 RA Kramer E.M., Dorit R.L., Irish V.F.;
 RT Molecular evolution of genes controlling petal and stamen
 RT development: duplication and divergence within the APETALA3 and
 RT PISTILLATA MADS-box gene lineages.";
 RL Genetics 149:765-783(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AF052874; AAC42589.1; -.

DR HSSP; P11746; 1MM.
 DR TRANSFAC; T03139; .
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01466; K-box; 1.
 DR Pfam; PF00319; SRF-TE; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SO SEQUENCE 228 AA; 26501 MM; 22405D9783465CE5 CRC64;

Query Match 51.2%; Score 623; DB 10; Length 228;
 Best local similarity 54.2%; Pred. No. 9, 1e-41;
 Matches 128; Conservative 38; Mismatches 58; Indels 12; Gaps 4;

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 DB 61 SLNGNTKRYVDKYQLSGISIMNSHYESLQNALNKQKINRRLREIRQRMGEDLDLTI 120
 QY 119 DELASLDDEMSSLDARQKRYVTKQTETTKKRYKNLEQRGNMLHGTFDEALAGDP 178
 DB 121 EELRSLEQNLEASVYKVRDRKHVILITQETTRKLNHTEQNHGLREF--EPILDEDP 178
 QY 179 QYGEDNEGDYESALALSNANNLYTFHLH--HPNLHGSSSLGSSITHLHDRLA 232
 DB 179 HYVIAHQEEDYESALIELAHGPNIFAFRLPQPNLHNGG-----YNCHDIRLA 228

Search completed: September 27, 2004, 09:28:17
 Job time : 76.7383 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 04:52:23 ; Search time 3964.76 Seconds
(without alignments)
2336.240 Million cell updates/sec

Title: US-10-069-527-4

Perfect score: 1216

Sequence: 1 MARKKIEIKIENQTNQVT.....HHGSSLSGSIYTHLDRLA 232

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delcp 6.0 , Delcxt 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALLIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCT -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-BEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1203	98.9	1102	8	MD0251116
2	1072.5	88.2	1043	8	AB081093
3	882.5	72.6	1014	8	AB055966
4	721.5	59.3	906	8	GHY9724
5	721.5	59.3	994	8	AF230704
6	709.5	58.3	681	6	AR372459
7	709.5	58.3	946	6	AR372458
8	690.5	56.8	895	6	LEIDR6
9	690.5	56.8	945	8	AY098734
10	667.5	54.9	938	8	AMDEFI
11	659	54.2	939	8	AF230703
12	641.5	52.8	881	8	PHGP
13	638	52.5	1113	8	NTMADSBOX
14	624.5	51.4	924	8	STPD4
15	623.5	51.3	965	8	ALFMBP
16	623	51.2	1008	8	AF052874
17	616.5	50.7	1005	6	AX478039
18	616	50.7	1005	8	AB071378
19	612	50.3	1039	8	AF503913
20	612	50.3	1129	8	AB099875
21	608.5	50.0	830	8	AY397762
22	600.5	49.4	833	8	AF209729
23	597	49.1	1002	8	AB094965
24	595	48.9	852	8	AB050649
25	590.5	48.6	952	8	AB094964
26	577	47.5	1016	8	AB094966
27	575	47.3	875	8	AF180364
28	575	47.3	839	8	AB090863
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35	566	46.5	687	8	AF180365
36	566	46.5	785	8	AF052875
37	564	46.4	730	8	AY142590
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39	564	46.4	1010	8	ATHAPETELA
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41	562.5	46.3	921	8	AY173060
42	562	46.2	976	8	SLSM3
43	561.5	46.1	763	8	AY173064
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ALIGNMENTS

RESULT 1

MD0251116 1102 bp mRNA linear PLN 16-NOV-2001
 LOCUS MD0251116
 DEFINITION Malus domestica mRNA for B-type MADS box protein (mads13 gene).
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 VERSION AJ251116.1 GI:16973293
 KEYWORDS B-type MADS box protein; mads13 gene.
 SOURCE Malus x domestica (apple tree)
 ORGANISM Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; euroside I; Rosales; Rosaceae; Maloideae; Malus.
 REFERENCE 1
 VORMAN, B. and SMULDERS, M.J.M.
 TITLE Isolation of apple B- and C-type MADS box genes from vegetative
 tissue
 JOURNAL unpublished
 REFERENCE 2 (bases 1 to 1102)
 AUTHORS van der Linden, C.G.
 TITLE Direct Submission
 JOURNAL Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic
 Diversity, CPRO Wageningen University & Research Centre, PO Box 16,
 Wageningen, 6700 AB, NETHERLANDS
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 Score: 1203.00 Matches: 230
 Percent Similarity: 99.14% Conservative: 0
 Best Local Similarity: 99.14% Mismatches: 2
 Query Match: 98.93% Indels: 0
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 QY 41 AlAlaYValSerIleuIleuLeuSerAsnThrAsnLysVechIseGluTyrIleSerPro 60
 Db 191 GCCAAGGCTCCCTCATATGCTCTCCAAACAAATTAATTAATGACAGATATACAGCCCT 250
 QY 61 ThrThrThrIysSerMetIYrAspAspIYrGlnIleYsThMeGlyIleAspLeuTyr 80
 Db 251 ACCACTACGACCAAGAGTATGATGACTATCAGAAAACHTATGGGATCATCTGTGG 310
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 QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
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 QY 121 LeuAlaSerLeuAspAsnGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 Db 431 CTGGCTTCTCTTGACGATGATGATGATGATCTTCTTGATGATGATGATGATGATGATG 490
 QY 141 HisValIleIleYsThrGlnThrGluThrThrIysLysIysValLysAsnLeuGluArg 160
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 QY 181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 Db 611 GGTATGAGACATGAGGAGACTACGAATCTGATGATGATGATGATGATGATGATGATGATG 670
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 QY 221 SerSerIleThrHisLeuHisAspLeuArgLeuAla 232
 Db 731 TCTTCATTAATCTCATCTGACAGATCTCGCTTCTCT 766
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 LOCUS AB081093
 DEFINITION Malus x domestica MdTM6 mRNA for MADS-box protein, complete cds.
 ACCESSION AB081093
 VERSION AB081093.1 GI:22775407
 KEYWORDS
 ORGANISM
 SOURCE
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; euroside I; Rosales; Rosaceae; Maloideae; Malus.
 REFERENCE 1
 MATSUMOTO, S., OHTSUBO, T. and SOEJIMA, J.
 TITLE Cloning and sequencing of apple MADS-box genes 'Md12P', 'MdTM6', and
 'MdMADS13'
 JOURNAL unpublished
 REFERENCE 2 (bases 1 to 1043)
 AUTHORS Ohtsubo, T. and Matsumoto, S.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,
 Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu,
 Gifu 501-1193, Japan (E-mail: shmatsumo@gcc.gifu-u.ac.jp,
 Tel:81-56-293-2257, Fax:81-56-293-2207)
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ORIGIN

Alignment Scores: 4.02e-89 Length: 1043
Pred. No.: 1072.50 Matches: 211
Score: 91.67% Conservative: 9
Percent Similarity: 87.92% Mismatches: 9
Best Local Similarity: 88.20% Indels: 11
Query Match: 8 Gaps: 3

US-10-069-527-4 (1-232) x AB081093 (1-1043)

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DB 123 TACTCCAGAGAGAGAAATGGATCTTCAGAAAGCTCAGAGCTCACCGTTCTGTGAT 182
QY 41 AlAlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 183 GCCAAGGCTCCCTCATCATGCTCTCCAACTAGTAAATGACAGATATATCAGCCCT 242
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyLeuAspLeuTyr 80
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DB 594 TGTATGTGGCAATGAGGAGAGATGATGATGATGATGATGATGATGATGATGATG 653
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DB 654 AACTTGACACTTTCAGCTCCACCGCACTCCGACCAAGCTCCACCACTTACCTTCAC 713
QY 213 HisHisGlyLysSerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeuAla 232
DB 714 CACCAACAGAGAGATGCTCGCTCGCTCCCTCCATCATCATCATCATCATCATCATCAT 773
RESULT 3
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LOCUS ROSA rugosa MASAKO B3 mRNA for MADS-box protein, complete cds.
DEFINITION
AB055966
ACCESSION
AB055966.1 GI:15216292
VERSION
KEYWORDS
SOURCE
ORGANISM
Rosa rugosa
Rosa rugosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE

1 Kitahara, K., Hirai, S., Fukui, H. and Matsumoto, S.
Rose MADS-box genes 'MASAKO B3' and B3' homologous to class B floral
identity genes
Plant Sci. 161, 549-557 (2001)
2 (bases 1 to 1014)
Matsumoto, S., Hirai, S. and Kitahara, K.
Submitted (19-FEB-2001) Shogo Matsumoto, Gifu University,
Department of Biology, Faculty of Education, 1-1, Yansigido, Gifu,
Gifu 501-1193, Japan (E-mail: shmatsumo@cc.gifu-u.ac.jp,
Tel:81-58-293-2257, Fax:81-58-293-2207)

FEATURES

source

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ORIGIN

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Percent Similarity: 72.16% Mismatches: 32
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Query Match: 8 Gaps: 3

US-10-069-527-4 (1-232) x AB055966 (1-1014)

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DB 105 TATTCAGACGAGAAATGGATGATGATGATGATGATGATGATGATGATGATGATG 164
QY 41 AlAlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 165 GCTCAGTCTCTCTCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 224
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyLeuAspLeuTyr 80
DB 225 ACCACTACGACCAAGAGATGTTGATCTCTCCAGAAAGATTTACAGATCATCATG 284
QY 81 ArgThrHisGluLysSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB 285 AGCTCACTACAGAGCAATGAAAGAACTTGTGAAACTGAAGAGCTTAACATTAAG 344
QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLysSerPheAspGlu 120
DB 345 CTGAGAGAGGACATCAGCAAGAGCTGGGCGCATGATCTTAATGCTGTGATGCTGAG 404
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB 405 CTCAGAGATCTGGAGAAACGATGATGATGATGATGATGATGATGATGATGATGATG 464

ORGANISM

Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Petunia.

REFERENCE

1 (bases 1 to 994)
Kramer, E.M. and Irish, V.F.
Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms
Int. J. Plant Sci. (2000) In press

2 (bases 1 to 994)
Kramer, E.M. and Irish, V.F.
Direct Submission
Submitted (03-FEB-2000) MDCB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA

FEATURES

source location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 5,386-57 Length: 994
Score: 721.50 Matches: 142
Percent Similarity: 74.36% Conservative: 32
Best Local Similarity: 60.68% Mismatches: 49
Query Match: 59.33% Indels: 11
DB: 8 Gaps: 4

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QY 41 AlaIysValSerLeuIleMetLeuSerAsnThrAsnIleMetHisGluTyrIleSerPro 60
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DB 301 CTAAGAGAGAGATTAAGCAAGAACAGGCAAGCAATGAGCGGCTCAATTTGACAGAA 360
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QY 141 HisValIleIleValThrGlnThrGlnThrIleIleIleValIleAsnLeuGlnGlnArg 160

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DB

649 TTGTGTTCT-----CGTGAATCAAGTCTTGCT 675

RESULT 6

AR372459

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

ATTNORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

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Pred. No.: 4,266-56 Length: 681
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Query Match: 58.35% Indels: 21
DB: 6 Gaps: 5

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DB 241 GGCATCTAATACAGAAATGCAAGAAATGCAAACTTGAACATTTGAAGATATCAATACAG 300
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DB 301 CTAAGAGAGAGATTAAGCAAGAACAGGCAAGCAATGAGCGGCTCAATTTGACAGAA 360

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Oy		141	HisValIleLysStrGlnThrGlnThrThylsLysValLysAsnDeuGluglnArg	160
Db		421	CATGTGATCAAACAACAAAACGAAGCCTTAACAGAAGAGGTGAAGATTATGAGGAGAGA	480
Oy		161	ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyLysProGlnTyr	180
Db		461	CATGAAACCCTTGATGATGGAATAT-----GAGCAAAACTAAGAGATGCACAGAT	531
Oy		181	GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaasn	200
Db		532	GGTTTAGTGACCAT-----GAGCTGCTGTTCGACTTCCAATGGGGCTTCC	579
Oy		201	AsnLeuTyrThrPheHisLeuHisHis-----ProAsnLeu	212
Db		560	AACCTCATAGCATTCGCCCTGCATCACGGGACACACCACCACCATCTCCATACTT	639
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DEFINITION	Sequence 2 from patent US 6395892.			
ACCESSION	AR372458			
VERSION	AR372458.1	GI:14609785		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 946)			
TITLE	Straus,S.H., Rottmann,W., Brunner,A. and Sheppard,L.			
JOURNAL FEATURES	Floral homeotic genes for manipulation of flowering in poplar and other plant species			
Patent:	US 6395892-A 2 28-MAY-2002;			
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Db	580	AACCTCTATGCAATTCGGCTCATCAGGAGCAACCAACCAACCATCTCCATATCTT	639
Qy	213	HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu	231
Db	640	CACCTT---GGAATGATGATTTGAGACC-----CATGAATCTCGCCTT	678
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ACCESSION	X60759		
VERSION	X60759.1 GI:19385		
KEYWORDS	MADS box; TDR6 gene.		
SOURCE	Lycopersicon esculentum (tomato)		
ORGANISM	Lycopersicon esculentum (tomato)		
REFERENCE	Pinell, L., Abu-Abeid, M., Zamir, D., Nacken, W., Schwarz-Sommer, Z. and Litschitz, E.		
AUTHORS	The MADS box gene family in tomato: temporal expression during floral development, conserved secondary structures and homology with homeotic genes from Antirrhinum and Arabidopsis		
JOURNAL	Plant J. 1 (2), 255-266 (1991)		
COMMENT	Submitted (01-JUL-1991) L. Pinell, Dept of Biology, Technion-Israel Inst of Technology, Haifa 32000, ISRAEL		
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Best Local Similarity: 59.74% Mismatches: 53
Query Match: 56.78% Indels: 11
DB: 8 Gaps: 4
US-10-069-527-4 (1-232) x LENDR6 (1-895)

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RESULT 9
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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MEDLINE
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REFERENCE
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COMMENT
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FEATURES
SOURCE

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ORIGIN
Alignment Scores:
Pred. No.: 3.49e-54 Length: 945
Score: 690.50 Matches: 138
Percent Similarity: 72.73% Conservative: 30
Best Local Similarity: 59.74% Mismatches: 52
Query Match: 56.78% Indels: 11
DB: 8 Gaps: 4
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DB 61 AGAAGAAACGGTATTTTCAAGAAACGTAAAGAACTTACTGTTCTTGACGCTAAGATC 120
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[illegible]

ORIGIN

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US-10-069-527-4 (1-232) X AMDEFI (1-998

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RESULT 11

AF230703

LOCUS

DEFINITION

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partial cds.

AF230703

939 bp

mRNA

linear

PLN 02-JUN-2000

VERSION AF230703.1 GI:8163947
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 SOURCE Hydrangea macrophylla
 ORGANISM Hydrangea macrophylla
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 asterids; Cornales; Hydrangeaceae; Hydrangea.
 REFERENCE
 AUTHORS Kramer, E.M. and Irish, V.F.
 TITLE Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms
 JOURNAL Int. J. Plant Sci. (2000) In press
 REFERENCE 2 (bases 1 to 939)
 AUTHORS Kramer, E.M. and Irish, V.F.
 TITLE Direct Submission
 JOURNAL Submitted (03-FEB-2000) MDCB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA
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 Pred. No.: 2,666-51 Length: 939
 Score: 659.00 Matches: 130
 Percent Similarity: 74.16% Conservative: 25
 Best Local Similarity: 62.20% Mismatches: 44
 Query Match: 54.19% Indels: 10
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QY 166 HlsGlyTyPheaspGlnGlnAlaIleargGlnArlenglyVhisValleuThr 185
 DB 418 -----TTCCTGATGAGAGAGAAATGTGAAGATCCACAGTACGATTAAGTGAAGAAC 471
 QY 186 GlnGlyAspTyrglnlysmethesgllyleaspleuThThThThThThTh 205
 DB 472 GAGGAGAGATGATGATCTGCTGCTGATTCGGAATAGGCTCCGATTCGATGCTTTC 531
 QY 206 HlsLeuHis-----HisProAsnLeuHisHlsGlyTyPheaspGlnGlnAla 223
 DB 532.GGCTTCACACCTTAATCTTACCATGAGAGAGTGGAGATATGATCA----- 585
 QY 224 ThHlsLeuHisAspleuThleuAla 232
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 LOCUS P.hydrida mRNA for sp. 881 bp mRNA linear PLN 06-OCT-1994
 DEFINITION
 ACCESSION X69346
 X69346.1 GI:22664
 VERSION
 KEYWORDS developmental gene; DNA-binding transcription factor; gp gene.
 SOURCE
 ORGANISM
 Petunia x hybrida
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Petunia.
 REFERENCE
 AUTHORS Kush, A., Brunelle, A., Shevell, D. and Chua, N.H.
 TITLE The cDNA sequence of two MADS box proteins in Petunia
 JOURNAL Plant Physiol. 102 (3), 1051-1052 (1993)
 MEDLINE 94105323
 PUBMED 8278527
 REFERENCE
 2 (bases 1 to 881)
 AUTHORS Brunelle, A.N.
 TITLE Direct Submission
 JOURNAL Submitted (23-NOV-1992) A.N. Brunelle, The Rockefeller University,
 Dept of Plant Molecular Biology, 1230 York Avenue, New York, NY
 10021, USA
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 ORIGIN
 Alignment Scores:
 Pred. No.: 9,886-50 Length: 881
 Score: 641.50 Matches: 129
 Percent Similarity: 71.12% Conservative: 36
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 Query Match: 52.75% Indels: 15
 DB: 8 Gaps: 4

US-10-069-527-4 (1-232) x PHCP (1-881)

QY 1 Metalaarglyylsiegliulelysleuileglusenglnthraanaarglnvalthr 20
 DB 18 ATGGCTCGTGAAGAATCCAGATCAAGAGATAGAAAACCAACCAACAGCAAGTACA 77
 QY 21 Tyrserysaagaagaanglyllephelysalslaingluileuthrvalleucysasp 40
 DB 78 TATCTAAGAGAAAGAAATGACCTTTCAAGAAAGCTAATGAACTGCTGTTTGGAT 137
 QY 41 Alalysvalserleulemetleuserasnthrasnlysmethisgluylrileserpro 60
 DB 138 GCCAAGATTCCATATATATGATTTCCAGTACTCGCAAGCTTCATGATCATTAAGCCA 137
 QY 61 Thrthrthrthrlyssermettyraspsptyrglnlysthrmetgillyleapleutrp 80
 DB 198 TCTATCAGACTAAGCAAGCTTGTGATCTGATCCAAAGACTGTGGAGTTGATCTTTGG 257
 QY 81 Argthrhisgluglusermetleuasptthrleutrpilsleuylsgluileasnauly 100
 DB 258 AACTCCCACTATGAGAAATGCAAGACCACTGAGAAAGCTAAAGAGTAATAGGAAT 317
 QY 101 Leuargargluilearglnargleuglyhisaspleuasnglyleuserpheaspjlu 120
 DB 318 CTCGGAAGAGATCAGGACAGAGATGGAAGAAAGCTTAACGATCTGAATGAGCAAG 377
 QY 121 Leualseleuaspaapglumerglnserleuaspaalalearglnarglylethr 140
 DB 378 TTGGAAGAGCTCATGAGAAATGTCAGCAATCTCTCAAGCTTATGCTGAAGAAAGTAT 437
 QY 141 Hisvallelysthrthrthrthrthrthrlyslslylevalysleuasnleuglnarg 160
 DB 438 AAGGTGATGGCAATCAGATTCAGATTCAGCAAGAGTCAAGAGATGGAAGAAAT 497
 QY 161 Argglysmetleuhsiglytyrphaspglinsulalaaglylusprrpoglnlyr 180
 DB 498 CATGGAATCTCTG-----CTTGAATTTGATGCAAGACCAAGCACTAAT 545
 QY 181 Glytyrgluspasnnglylaspptyrglnseraleuaspaaleusernglylaasn 200
 DB 546 GGGCTAGTGAACAAGAGTGAATCAATCTGTGCTTTCCTTCCAAATGAGGGCAT 605
 QY 201 Asnleutythrphesileu-----Hisshpsoaleu 212
 DB 606 CGCATATTAACCTTACCTTCAACCAACCAACCAACCAATCATCATCTT 665
 QY 213 Hishtslyglserleuileuglyserlethr 224
 DB 666 CACAGTGTGGA-----GGCTCTGATATCACT 692
 RESULT 13
 NTMADSBOX 1113 bp mRNA linear PLN 06-FEB-1997
 LOCUS N tabacum mRNA for MADS-box protein.
 DEFINITION X96428
 ACCESSION X96428.1 GI:1370275
 VERSION MADS-box protein.
 KEYWORDS Nicotiana tabacum (common tobacco)
 SOURCE Nicotiana tabacum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterides; lamids; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1
 AUTHORS Davies, B., Di Rosa, A., Eneva, T., Saedler, H. and Sommer, H.
 TITLE Combinations of tobacco floral organ identity by expression of
 JOURNAL Plant J. 10 (4), 663-677 (1996)
 MEDLINE 97048712
 PUBMED 8893543
 REFERENCE 2 (bases 1 to 1113)
 AUTHORS Davies, B.
 TITLE Direct Submission

JOURNAL

Submitted (05-MAR-1996) B. Davies, MEIZ-KOELN, PLANT MOLECULAR
 GENETICS, CARL-VON-LINNE WEG 10, D-50829 KOELN, FRG

FEATURES

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CDS

ORIGIN

Alignment Scores:

	Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Percent Similarity:	72.05%		56.33%				
Best Local Similarity:	52.47%						
Query Match:	8						5

US-10-069-527-4 (1-232) x NTMADSBOX (1-1113)

QY 1 Metalaarglyylsiegliulelysleuileglusenglnthraanaarglnvalthr 20
 DB 125 ATGGCTCGTGAAGAATCCAGATCAAGAGATAGAAAACCAACCAACAGCAAGTACA 184
 QY 21 Tyrserysaagaagaanglyllephelysalslaingluileuthrvalleucysasp 40
 DB 185 TATCTAAGAGAAAGAAATGACCTTTCAAGAAAGCTAATGAACTGCTGTTTGGAT 244
 QY 41 Alalysvalserleulemetleuserasnthrasnlysmethisgluylrileserpro 60
 DB 245 GCTAAGTTTCTATATATATGATTTCAAGTACCGCAACCTTCAATTTATTAAGTCCC 304
 QY 61 Thrthrthrthrlyssermettyraspsptyrglnlysthrmetgillyleapleutrp 80
 DB 305 TCTGTACAGACCAAGCAAGTGTGATCTGATCAAGAGAGCTGTGAGATTTGG 364
 QY 81 Argthrhisgluglusermetleuasptthrleutrpilsleuylsgluileasnauly 100
 DB 365 AACTCCCACTATGAGAAATGCAAGACCAAGTGAAGAAAGCTTAAGATAGGAAT 424
 QY 101 Leuargargluilearglnargleuglyhisaspleuasnglyleuserpheaspjlu 120
 DB 425 CTCGGAAGAGATCAGGACAGAGATGGAAGAAAGCTTAACGATCTGAATGAGCAG 484
 QY 121 Leualseleuaspaapglumerglnserleuaspaalalearglnarglylethr 140
 DB 485 TTGGAAGAGCTCATGAGAAATGTCAGCAATCTCTCAAGCTTATGCTGAAGAAAGTAT 544
 QY 141 Hisvallelysthrthrthrthrthrthrlyslslylevalysleuasnleuglnarg 160
 DB 545 AAACTGATTTGCAATCAGATTCATCAACCAAGAGCTGAGATGGAAGAAATA 604
 QY 161 Argglysmetleuhsiglytyrphaspglinsulalaaglylusprrpoglnlyr 180
 DB 605 CATGGAATCTATTTG-----CTTGAATTTGATGCAAGACCAAGAGATCCA---TAT 652
 QY 181 Glytyrgluspasnnglylaspptyrglnseraleuaspaaleusernglylaasn 200
 DB 653 GGATTCGTTGACCAAGAGGAGCTAATTAATCTGTGCTTGGATTTCCAAATGAGGGCGG 712

Accession	Source	Organism	Gene	Protein	Length	Score	Align	Score	Align
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713	CGCATATTATAGGCTTACGGCTTCACCAACCAACCAACGCAATATCATCATCTTCACAGTGA	772							
216	GlySerSerLeuGlySerSerIleThr	224							
773	CGA-----GGCTCCGATATCACT	790							
STPD4	STPD4	924 bp	mRNA	linear	PLN 12-UU-1994				
DEFINITION	S.tuberosum def4 mRNA for deficiens analogue (clone pd4).								
ACCESSION	X67508								
VERSION	X67508.1								
KEYWORDS	def4 gene; deficiens; MADS-box protein; transcriptional activator.								
SOURCE	Solanum tuberosum (potato)								
ORGANISM	Solanum tuberosum								
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.								
AUTHORS	1 (bases 1 to 924)								
TITLE	Garcia-Maroto, F., Salamini, F. and Rohde, W.								
JOURNAL	Molecular cloning and expression patterns of three alleles of the Deficiens-homologous gene St-deficiens from Solanum tuberosum								
MEDLINE	Plant J. 4 (5), 771-780 (1993)								
PMID	9410091								
REFERENCE	2 (bases 1 to 924)								
AUTHORS	Maroto, Salamini and Rohde.								
JOURNAL	Unpublished								
AUTHORS	3 (bases 1 to 924)								
TITLE	Garcia-Maroto, F.								
JOURNAL	Direct Submission								
PMID	Submitted (24-AUG-1992) F. Garcia-Maroto, MPI f								
REFERENCE	Zuechtungsforchung, Carl-von-Linne-Weg 10, 5000 Koeln 30, FRG								
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Query Match: 51.36% Indels: 11
DB: 8 Gaps: 3
US-10-069-527-4 (1-232) x STPDA (1-924)

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QY	21	TyrSerIysAspAspAsnGlyIlePheIleValIaGlnGluLeuThrValLeuCysAsp	40
DB	95	TATTCAAAGAAAGAAAATGGGCTTATTCAGAGGCTAATGAACCTTACGTTCTTGTGAT	154
QY	41	AlaIysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro	60
DB	155	GCTAAAGTTTCATATGTTATGATTTCTAGTACTGGAAAACCTCATGATTTATTAAGTCCC	214
QY	61	ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp	80
DB	215	TCCTATCAGCAACAATTTGTTGATCTGTACCAAAAGACTATTGGAGTTGATATTTGG	274
QY	81	ArgThrHisGluGluSerMetLysAspThrLeuTrpLysLeuLysGluIleAsnAsnLys	100
DB	275	ACTCTTCCTCTATGTGAAGAAATCCAGAGAGCTGGAGAACTTAAAGATTTAAATAGCAT	334
QY	101	LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu	120
DB	335	CTACGAAAGAGATCAGGCAAGAGATGGGAAGAAAGCCCTAAATGATCTGAACCTTGAACAG	394
QY	121	LeuAlaSerLeuAspAspGluMetClnSerSerLeuAspAlaIleArgGlnArgLysTyr	140
DB	395	TTGAAAGAGCTCAGAGAAATGTGACATTTCTGAAAGCTTATTCGTGAAGAAAGATAT	454
QY	141	HisValIleLysThrGlnThrGluThrThrLysLysValLysAsnLeuGluIleArg	160
DB	455	AAGGTGATGGCAATCAGATGGAACCTTACAGAAAGAGTTAGGAATGTGGAAGAATA	514
QY	161	ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyGluAspProGlnTyr	180
DB	515	CATGAAATTCCTCCG-----CTTGAATTATGCAAGACAGAGATCCATATGCT	565
QY	181	GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn	200
DB	566	GGATTAGTTGGACAGAGAGACTACATTCCTGCTGATGCCACATCGAGGGCAT	625
QY	201	AsnLeuTyrThrPheHisLeu-----HisHisProAsnLeuHisGly	215
DB	626	CATATATTAGCCTTAGGCTTCACCAACAAACATCATCATCATCTTCACAGTGA	685
QY	216	GlySerSerLeuGlySerSerIleThr	224
DB	686	GGT-----GGCTGTGATTTACT	703

RESULT 15	LOCUS	ALFMBP	965 bp	mRNA	linear	PLN 05-MAR-1997
DEFINITION	Medicago sativa (clone nmh7)	MADS-box protein mRNA, complete cds.				
ACCESSION	L41727	L41727.1	GI:1870205			
VERSION						
KEYWORDS	MADS box protein.					
SOURCE	Medicago sativa					
ORGANISM	Medicago sativa					
REFERENCE	1 (bases 1 to 965)					
AUTHORS	Heard, J. and Dunn, K.					
TITLE	Symbiotic induction of a MADS-box gene during development of alfalfa root nodules					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	92 (12),	5273-5277	(1995)		
MEDLINE	95296822					
PUBMED	7777496					

REFERENCE 2 (bases 1 to 965)

AUTHORS Dunn, K.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-1997) Biology, Boston College, Chestnut Hill, MA 02167, USA

COMMENT On Mar 5, 1997 this sequence version replaced gi:780292.
 FEATURES location/Qualifiers

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CDS

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Alignment Scores:

Pred. No.: 4,93e-48 Length: 965
 Score: 623.50 Matches: 123
 Percent Similarity: 69.91% Conservative: 35
 Best Local Similarity: 54.42% Mismatches: 63
 Query Match: 51.27% Indels: 5
 DB: 8 Gaps: 2

US-10-069-527-4 (1-232) x ALFBP (1-965)

QY 1 MetAlaArgGlyLysIleGluIleValLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 1 ATGCTCGAGAGAAAGATCCAGATTAGAGAGTAGAGAACACAGACAGCAAGTAAATC 60
 QY 21 TySerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
 Db 61 TACTCAAAACGAGAGATGCTCTTTTCAGAGAGCCATAGCTCACTGTTCTTGTGAT 120
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
 Db 121 GCTAAGGTTTCTATTATCATGTCTCCAGCATGGCAAGCTTCATGATATACATTAGCCCC 180
 QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
 Db 181 TCGCCCTCAACAAAGCATTTTCGATCAATATCAGACGCTGAGAAATGATCTGTGG 240
 QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
 Db 241 AACTCTCATATGAGATATGACAGAGAACTTGAAGAACTGAAAGACCTCAATTAGGAT 300
 QY 101 LeuArgArgGluIleArgIleArgLysHisAspLeuAsnGlyLeuSerPheAspGlu 120
 Db 301 CTTCGCAAGAGATTGGCAGAGGAGGAGGAGATGCTGATATCATCTGAGCATGAGAGAG 360
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 Db 361 CTGAGGCTTCTTGAAGATGAATGACAGAGCTCTCAAGCTATTTGTAAGCGCAGATAT 420
 QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160

Db 421 AAGTGATTAACAATCATGATTGACACCCAAAGAAAGATTAAATATGACAGAGAGGTC 480
 QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyGluAspProGlnTyr 180
 Db 481 GACAAACAGACTCTGCGT-----GACTTGATGACAGAGAGAAAGATCCAGCTTT 531
 QY 181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 Db 532 GAATGATGACAAATGAGAGGAGATGAGCTGTGATTTGATTCTCAAAATTTAGGTCCA 591
 QY 201 AsnLeuTyrThrPheHisLeuHis-----HisProAsnLeuHisHisGlyLysSerSer 218
 Db 592 CGCATGTTTGATTTGAGCTTACAGCTTACTATCTCATCTCAATATGAGAGAGATCA 651
 QY 219 LeuGlySerSerIleThr 224
 Db 652 GCTGCCCTGGAATCTCACC 669

Search completed: September 26, 2004, 09:11:16
 Job time : 3968.76 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OW protein - nucleic search, using frame_plus_pzn model

Run on: September 26, 2004, 02:46:48 ; Search time 389.781 Seconds
(without alignments)
2528.555 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
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Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
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Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1216	100.0	982	4	AA000104
2	709.5	58.3	681	4	AA085393
3	709.5	58.3	946	4	AA085393
4	709.5	58.3	946	6	ABK88485
5	709.5	58.3	946	8	ACA62518
6	701.5	57.7	924	3	AA257943
7	641.5	52.8	882	2	AA051189
8	616.5	50.7	926	6	AA042259

9	585.5	48.1	989	3	AA055879	AA055879 Eucalyptu
10	569	46.8	959	3	AA040831	AA040831 Arabidops
11	564	46.4	954	3	AA051525	AA051525 Arabidops
12	564	46.4	1170	3	AA051790	AA051790 Arabidops
13	553.5	45.5	1257	6	AA042257	AA042257 Corn AP3
14	545.5	44.9	954	3	AA040685	AA040685 Arabidops
15	455.5	37.5	409	3	AA063790	AA063790 Eucalyptu
16	419.5	34.5	4285	4	AA085391	AA085391 Nucleotid
17	419.5	34.5	4285	6	ABK88484	ABK88484 Poplar pr
18	419.5	34.5	4285	8	ACA62517	ACA62517 Poplar ho
19	419	34.5	386	3	AA057268	AA057268 Eucalyptu
20	411.5	33.8	4192	3	AA057942	AA057942 Poplar fl
21	410.5	33.8	905	3	AA057024	AA057024 Eucalyptu
22	367	30.2	868	4	AA050103	AA050103 Granny Sm
23	334	27.5	269	3	AA06754	AA06754 Sucalypu
24	331.5	27.3	896	9	ADD55880	ADD55880 Thalecres
25	331.5	27.3	947	3	AA039436	AA039436 Arabidops
26	326	26.8	780	2	AA055089	AA055089 FBPI CDNA
27	326	26.8	10139	6	AB081397	AB081397 Truncated
28	313.5	25.8	780	6	ABK82086	ABK82086 Novel fl
29	313.5	25.8	783	6	ABK82087	ABK82087 Novel fl
30	313.5	25.8	1065	6	ABK82124	ABK82124 DNA encod
31	312.5	25.7	1065	6	ABK82127	ABK82127 DNA encod
32	311.5	25.6	909	3	AA035208	AA035208 Arabidops
33	310.5	25.5	764	6	ABK82089	ABK82089 Novel fl
34	310.5	25.5	783	6	ABK82088	ABK82088 Novel fl
35	310.5	25.5	789	6	ABK82085	ABK82085 DNA encod
36	310.5	25.5	979	6	ABK82123	ABK82123 DNA encod
37	308.5	25.4	1089	6	AA042258	AA042258 Corn AP3
38	305.5	25.1	1268	4	AA076058	AA076058 Maize MAD
39	305.5	25.1	1268	5	AA076445	AA076445 Maize ZmM
40	305.5	25.1	1280	6	AA043930	AA043930 Corn nitr
41	302	24.8	582	6	ABK82090	ABK82090 Novel fl
42	298	24.5	1004	3	AA046623	AA046623 Zea mays
43	296.5	24.4	666	3	AA043001	AA043001 Arabidops
44	296.5	24.4	666	6	AB014637	AB014637 Arabidops
45	296	24.3	946	2	AA014920	AA014920 NCMA053 C

ALIGNMENTS

RESULT 1	AA000104	AA000104 standard; CDNA; 982 BP.
XX	AA000104	
AC	AA000104	
XX	AA000104	
DT	11-SEP-2003	(revised)
DT	17-MAY-2001	(first entry)
XX	XX	
DE	Granny Smith apple cDNA encoding MdAP3.	
XX	XX	
KW	Granny Smith apple; MdAP3; seedless fruit; horticulture;	
KW	accelerated breeding programme; cross pollination; transgenic plant;	
KW	biennial bearing tendency; coding moth; ss.	
XX	XX	
OS	Malus x domestica; var. Granny Smith.	
XX	XX	
FT	Key	Location/Qualifiers
FT	CDs	1..699
FT		/*tag= a
FT		/product= "MdAP3"
XX	XX	
PD	15-MAR-2001.	
XX	XX	
PF	07-SEP-2000; 2000MO-NC000176.	
XX	XX	
PR	07-SEP-1999; 99NZ-00337688.	
XX	XX	
PA	(HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.	
XX	XX	

CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility
 XX
 SQ Sequence 681 BP, 228 A; 148 C; 157 G; 148 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.35e-67	Length:	681
Score:	709.50	Matches:	149
Percent Similarity:	72.38%	Conservative:	24
Best Local Similarity:	62.34%	Mismatches:	45
Query Match:	58.35%	Indels:	21
DB:	4	Gaps:	5

US-10-069-527-4 (1-232) x AAF85393 (1-681)

```

QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 1 ATGGGCTCGTGGAAAGATTGAATCAAGAGATCGAAACCCCAACAGGCAAGTCACC 60
QY 21 TySerLysArgArgAsnGlyIlePheLysIleGlnGlnGlnLeuThrValLeuCysAsp 40
DB 61 TACTCGAAGAGAGAAATGATGATTTTCAAGAAAGCCCAAGAACTCACTGACTTGTGAT 120
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 121 GCTAAGGCTCTCTTATCATGTTCTTCAACACTCAACAACTCAAGATCAATTAGCCCC 180
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB 191 TCCACATCGACAAAGAAATGATCATGATCATATCAATCAAGAGCGTTAGGATGATCTGCG 240
QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrIleLysGluIleAsnAsnLys 100
DB 241 GGCACCTCATACGAAAGAAATGCAAGAGCCTTGAAGAGAGCTGAATGATATCATATAG 300
QY 101 LeuArgArgGlnIleArgGlnArgLeuGlnHisAspLysGlnLysLeuSerPheAspGlu 120
DB 301 CTGAACACAAAGAAATCAAGAGAGAGAGAGAGAGGCGCTGATGATCTAGCATTTGATCAT 360
QY 121 LeuAlaSerLeuAspAspGlnUeGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB 361 CTGCCCGGCTTGAACCAACATATGACTGAGCGCTTGAATGCGTGCCTGCGAGAGATAC 420
QY 141 HisValIleLysThrGlnThrGlnThrHisLysLysValLysAsnLeuGlnGlnArg 160
DB 421 CATGGATCAAAACCAAAACGAAACCTTACAGAAAGAGTGAAGAAATTTAGAGAGAGA 480
QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGlnAlaIleGlyLysAspProGlnTyr 180
DB 481 CATGGAACCTCTTGTATGATATAT-----GAAGCAAAACTAGAGATGACAGATAT 531
QY 181 GlyTyrGlnAspAsnGlnGlnLysAspTyrGlnUeSerAlaLeuAlaLeuSerAsnGlnLys 200
DB 531 GGTTTAGTGACAAAT-----GAAGCTGCTGTGCACTTGCAAAATGGGCGCTTCC 579
QY 201 AsnLeuTyrThrPheHisLeuHisHis-----ProAsnLeu 212
DB 580 AACCTCTATGATTCGCGCTGATCAACGGGCAACACACACACATCCTTATCTT 639
QY 213 HisHisGlyLysSerSerLeuGlnSerSerIleThrHisLeuHisAspLeuArgLeu 231
DB 640 CACCTT---GGAAGATGATTTGGAGCC-----CATGAACCTTGGCCTT 678

```

RESULT 3

AAF85392
 ID AAF85392 standard; cDNA, 946 BP.

AAF85392;

23-JUL-2001 (first entry)

Nucleotide sequence of the floral homeotic protein PTD.

XX

KM floral homeotic gene; PTD; PTLF; PTA-G-1; PTA-G-2; floral tissue; LEAFY;
 KM LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KM fertility; sterility; ss.

OS Populus balsamifera.

PH Key	Location/Qualifiers
FT CDS	1..684
FT	/*tag= a
FT	/product= "PTD"

PN CM2319853-A1.

PD 01-APR-2001.

PF 02-OCT-2000; 2000CA-02319853.

PR 01-OCT-1999; 99US-00410464.

PA (UYOR-) UNIV OREGON HEALTH SCI.

DR Rotman WH, Straus SH, Brunner AM, Shepard LA;

DX WPI; 2001-336098/36.

DR P-PSDB; AAB68435.

PT Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,
 PT particularly sterility.

PS Claim 25; Page 41-42; 69pp; English.

XX The present sequence encodes a floral homeotic protein, designated PTD.
 CC It is derived from Populus balsamifera subsp. trichocarpa. The
 CC specification also describes PTLF, PTA-G-1 and PTA-G-2 proteins. The floral
 CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of
 CC LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 CC primordia from the onset of organogenesis. PTA-G-1 and PTA-G-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility

XX Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.17e-67	Length:	946
Score:	709.50	Matches:	149
Percent Similarity:	72.38%	Conservative:	24
Best Local Similarity:	62.34%	Mismatches:	45
Query Match:	58.35%	Indels:	21
DB:	4	Gaps:	5

US-10-069-527-4 (1-232) x AAF85392 (1-946)

```

QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 1 ATGGGCTCGTGGAAAGATTGAATCAAGAGATCGAAACCCCAACAGGCAAGTCACC 60
QY 21 TySerLysArgArgAsnGlyIlePheLysIleGlnGlnGlnLeuThrValLeuCysAsp 40
DB 61 TACTCGAAGAGAGAAATGATGATTTTCAAGAAAGCCCAAGAACTCACTGACTTGTGAT 120
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 121 GCTAAGGCTCTCTTATCATGTTCTTCAACACTCAACAACTCAAGATCAATTAGCCCC 180
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB 181 TCCACATCGACAAAGAAATGATCATGATCATATCAAGAGCGTTAGGATGATCTGCTG 240
QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100

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Db 241 GGCACCTCAATACGAGAAATGCAAGAGCACTTGAGGAGAGCTGAATGATATCAATCATATAG 300
Qy 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db 301 CTGAGACAAAGAAATAGGACAGAGAGAGAGAGGCGCTGAAATGATCTGAGCATTTGATCAT 360
Qy 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLeuTyr 140
Db 361 CTGGCGGCTTTGAGCAACATATATGCTGAACCTTGATGCTGCTGGCAGAGAGATAC 420
Qy 141 HisValIleIleThrGlnThrGlnThrThrLysLysLysValLysAsnLeuGluGlnArg 160
Db 421 CATGGATCAAAACCAAAACCAAAACCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleArgGlnArgLeuTyr 180
Db 481 CATGAAACCTCTTCATGAGAAATAT-----GAAACCAAAACCTAGAGATCCAGCATAT 531
Qy 181 GlyTyrGluAspAspAspGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
Db 532 GATTTAGTGGACAAAT-----GAAAGCTGCTGTGCACTTGCAAAATGGGGCTTCC 579
Qy 201 AsnLeuTyrThrPheHisLeuHisHis-----ProAsnLeu 212
Db 580 AACCTCATATGATTCGCGCTGCATCAGGGCAACACACACACATCTCCCTAATCTT 639
Qy 213 HisHisGlyGlySerSerLeuGlySerSerLeuThrHisLeuHisAspLeuAlaGlu 231
Db 640 CACCTT---GGAGATGATGATTGGAGCC-----CATGAACTTCGCGCTT 678

RESULT 4
ABK88485
ID ABK88485 standard; cDNA, 946 BP.
XX
AC ABK88485;
XX
DT 29-AUG-2003 (revised)
DT 07-OCT-2002 (first entry)
XX
DE Poplar protein transduction domain, PTD, cDNA.
XX
KW Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;
KW protein transduction domain; floral homeotic gene;
KW floral-specific expression; cytochrome; fertility; sterility; PTLF;
KW PTA-1; PTA-2.
XX
OS Populus balsamifera; subsp. trichocarpa.
XX
FH Key Location/Qualifiers
FT 1..684
FT /*tag= a
FT /product= "PTD"
XX
PN US6395892-B1.
XX
PD 28-MAY-2002.
XX
PF 01-OCT-1999; 99US-00410464.
XX
PR 06-APR-1998; 98US-0080851P.
PR 06-APR-1999; 99US-00287700.
XX
FA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Straus SH, Rottmann W, Brunner A, Sheppard L,
XX
DR WPI: 2002-572853/61.
XX
DR P-PSDB; ABG30865.
XX
PT New protein transduction domain promoter nucleic acid molecule useful for
PT producing transgenic plants having modified fertility characteristics,
PT particularly sterility.

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XX
XX Example 1; Col 35-38; 46P; English.
XX
CC The invention relates to an isolated nucleic acid molecule especially a
CC protein transduction domain (PTD) promoter: (i) that hybridizes under
CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 % SDS (sodium
CC dodecyl sulphate) at 65 plus or minus 5 degrees Celsius comprising 35
CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
CC and is the homologue of DEFICIENS. Also included are a recombinant
CC nucleic acid comprising the PTD promoter, a cell transformed with the
CC recombinant nucleic acid and a transgenic plant comprising the
CC expression of genes such as cytochrome, that are employed in genetic
CC ablation strategies to produce trees having modified fertility
CC characteristics, including sterility. Genetic constructs comprising
CC antisense versions or dominant negative mutants of PTD are useful in
CC producing genetically engineered Poplar and other trees, and for sense
CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTA-1 and
CC PTA-2 (none are defined). The present sequence is the PTD cDNA. (updated
CC on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 5,176-67 Length: 946
Score: 709.50 Matches: 149
Percent Similarity: 72.38% Conservative: 24
Best Local Similarity: 62.34% Mismatches: 45
Query Match: 58.35% Indels: 21
DB: Gaps: 5

US-10-069-527-4 (1-232) x ABK88485 (1-946)
Qy 1 MetAlaArgGlyLysIleGluIleLeuLeuGlnGlnThrValThr 20
Db 1 ATGGGTCGTGGAAAGATGAAATGCAAGAGATCCAAACCAACCAAGAGAGAGAGAGAGAGAG 60
Qy 21 TyrSerLysArgArgAsnGlyIlePheLysLysLysLysLysLysLysLysLysLysLys 40
Db 61 TACTCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Qy 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlyTyrTyrTyr 60
Db 121 GCTAAGGCTCTCTTATCATATCTCTCAACCACTCAACCACTCAACCACTCAACCACTCAAC 180
Qy 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
Db 181 TCCACATGACAAAGAGAGATCTACGATCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuGlyLeuGlyLeuGlyLeu 100
Db 241 GGCACCTCAATACGAGAAATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db 301 CTGAGACAAAGAAATAGGACAGAGAGAGAGAGGCGCTGAAATGATCTGAGCATTTGATCAT 360
Qy 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLeuTyr 140
Db 361 CTGGCGGCTTTGAGCAACATATATGCTGAACCTTGATGCTGCTGGCAGAGAGATAC 420
Qy 141 HisValIleIleThrGlnThrGlnThrThrLysLysLysValLysAsnLeuGluGlnArg 160
Db 421 CATGGATCAAAACCAAAACCAAAACCACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleArgGlnArgLeuTyr 180
Db 481 CATGAAACCTCTTCATGAGAAATAT-----GAAACCAAAACCTAGAGATCCAGCATAT 531
Qy 181 GlyTyrGluAspAspAspGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
Db 532 GATTTAGTGGACAAAT-----GAAAGCTGCTGTGCACTTGCAAAATGGGGCTTCC 579

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Oy		20	AASleUvThrpheistshis-----Prostlen	21
Dd		580	AACCTTGATGCAATTCCGCCTCATCAGCGGACAACCACACACACATTCCTTACTTT	639
Oy		213	HASHIGLGYIYserSerLeuglYserSerilrhlrhIsleuHISAspleArgLeu	221
Dd		640	CACCTT---GGAGATGATTTGGAGGCC-----CATGAACCTTCGCCTT	678
		RESULT 5		
ID		ACA62518 standard; cDNA; 946 BP.		
XX		ACA62518;		
AC				
DT		18-AUG-2003 (first entry)		
DE		Poplar homeotic gene PTD, cDNA.		
KW		Poplar; ss; gene; PTD; deficiencies; homeotic gene; floral development;		
KM		sterile tree; pulp; paper; plant.		
XX				
OS		Populus balsamifera subsp. trichocarpa.		
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..684		
FT	FT	/tag= a		
FT	FT	/product= "PTD"		
XX		/note= "This CDS is specifically claimed in claim 1"		
PN		US2003033628-A1.		
PD		13-FEB-2003.		
PJ				
PF		21-MAR-2002; 2002US-00104580.		
XX				
PR		06-APR-1998; 98US-0080851P.		
PR		06-APR-1999; 99US-00287700.		
PR		01-OCT-1999; 99US-00410464.		
XX				
PA	(UYOR-) UNIV OREGON HEALTH SCI.			
PI	Strauss SH, Rottmann W, Brunner A, Shepard L;			
DR	WPt; 2003-466273/44.			
DR	P-PSDB; ABU61893.			
XX				
PT	New floral homeotic nucleic acid molecules, useful for the manipulation			
PT	of flowering in Poplar and other plant species, and for producing			
PT	transgenic plants having modified fertility characteristics, particularly			
PT	sterility.			
PS				
PS	Claim 1; Page 20-21; 48pp; English.			
CC	The invention relates to an isolated nucleic acid molecule comprising at			
CC	least 15 consecutive nucleotides of the gene, cDNA or coding sequence of			
CC	4 homeotic genes from poplar, PTDF (LEAFY and FLORICA homologue), PTD			
CC	(DEFICIENS homologue), and PRAG-1/PTA-2 (both homologues of AGAMOUS).			
CC	Also included are a recombinant nucleic acid molecule comprising a			
CC	promoter sequence operably linked to the nucleic acid molecule, a cell			
CC	transformed with the nucleic acid molecule, a transgenic plant comprising			
CC	the recombinant nucleic acid molecule and the purified proteins encoded			
CC	by the nucleic acids. The nucleic acid molecules are useful for the			
CC	manipulation of flowering in Poplar and other plant species, for			
CC	producing transgenic plants having modified fertility characteristics			
CC	(particularly sterility) and in the pulp and paper industries. The			
CC	present sequence is the poplar PTD cDNA			
SQ				
	Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;			
	Alignment Scores:			
	Pred. No.: 5.17e-67 Length: 946			
	Score: 709.50 Matches: 19			
	Percent Similarity: 72.38% Conservative: 24			

Best Local Similarity:	62.34%	Mismatches:	45
Query Match:	58.35%	Indels:	21
DB:	8	Gaps:	5
US-10-069-527-4 (1-232) x ACA62518 (1-946)			
Qy	1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr	20	
Db	1 ATGGGTCGTGAAAAGATTGAATCAAGAGATCGAAAACCCCAACAGAGCAATGACC	60	
Qy	21 TyrSerLysArgArgAsnGlyIlePheLysLysAlaGlnGlnLeuThrValLeuCysAsp	40	
Db	61 TACTCCAAAGAAAGAAAGTATTTTCAAGAAACCCCAAAAGCTCACTGACTTGTGAT	120	
Qy	41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnTyrIleSerPro	60	
Db	121 GCTAAGTCTCTTATCATGTCTTCCAAACATCAAACTCATAGTACATTAACCCC	180	
Qy	61 ThrThrThrThrLysSerMetCysTrpAspTyrGlnLysThrMetGlyIleAspLeuTrp	80	
Db	181 TCCACATCCACAAAGAAATCTACAGATCAAAATGACAAACCTTACGCAATGATCTGTGG	240	
Qy	81 ArgThrHisGlnGlnSerMetLysAspPheThrLeuTrpLysLeuLysGlnIleAsnLeuLys	100	
Db	241 GGCACCTCAATACGAGAAAATGCAAGAGCATTTGGAGAGCTGATATCATCATCAAG	300	
Qy	101 LeuArgArgGlnIleArgGlnArgGlnGlyHisAspLeuAsnGlyLeuSerPheAspGln	120	
Db	301 CTGAGCAAGAAATCAGGACAGGAGAGAGAGAGGCTGATGATCTGACATTGATCAT	360	
Qy	121 LeuAlaSerLeuAspAspGlnMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr	140	
Db	361 CTGCGGGCTTTGACCAACATATGACTGAAACCTTTGATGGGTGGCTGGCAGAGAACTC	420	
Qy	141 HisValIleLysThrGlnThrGlnThrThrLysLysLysValLysAsnLeuGlnGlnArg	160	
Db	421 CAGTGATATAAACACAAAGAAACCTACAGAGAAAGGTGAAGATTATGAGAGAGAG	480	
Qy	161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyLysAspProGlnTyr	180	
Db	481 CATTGAAACCTCTTATGGAATAT-----GAAACAAACTGAGGATCGACAGTAT	531	
Qy	181 GlyTyrGlnAspAsnGlnGlyLysPyrGlnSerAlaLeuLysSerAsnGlyAlaAsn	200	
Db	532 GGTTCATGTCGACAAAT-----GAACTCTGTTGCACTGCAATGGGGCTTCC	579	
Qy	201 AsnLeuTyrThrPheHisLeuHisHis-----ProAsnLeu	212	
Db	580 AACCTCTATGATTCGCGCTGCATCAGCGAGACACACACACACACCTCCCTAATCTTT	639	
Qy	213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLys	231	
Db	640 CACCTT--GGAAGATGATTTGGACC-----CATGAATTCGCTTT	678	
RESULT 6			
AAZ57943			
ID	AAZ57943 standard; cDNA; 924 BP.		
AC	AAZ57943;		
XX			
DT	11-APR-2000 (first entry)		
DE	Poplar floral homeotic gene PTD cDNA.		
XX			
KM	Poplar; PTD; floral homeotic gene; transgenic plant; sterility;		
XX	fertility; ss.		
OS	Populus balsamifera subsp. trichocarpa.		
XX			
FH	Location/Qualifiers		
FT	1..684		
FT	/note: "the coding region is also specifically claimed in		

Claim 1"

FT CA2227940-A1.
 XX 06-OCT-1999.
 XX 07-APR-1998; 98CA-02227940.
 XX 06-APR-1998; 98US-00080851.
 XX (UNIV OREGON HEALTH SCI.
 XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH,
 XX WPI; 2000-106662/10.
 XX P-PSDB; AAY58654.
 XX Nucleic acid from *Populus trichocarpa* genes, useful for producing
 PT transgenic plants, particularly trees, with modified fertility
 PT characteristics such as sterility.
 XX
 XX Claim 1; Page 46-47; 92pp; English.
 XX
 XX The present sequence is that of cDNA encoding *Populus balsamifera* subsp.
 CC *trichocarpa* PTD protein (see AAY58654). The PTD gene (see AA257942) is
 CC of 4 newly identified floral homeotic genes from this poplar species. It
 CC is a homologue of DBF1/EMS and is expressed strongly in stamen primordia
 CC from the onset of organogenesis, and is also expressed at low levels in
 CC carpel primordia. The invention provides nucleic acid sequences of these
 CC 4 *Populus* genes, the corresponding cDNA sequences (see AA257942-49) and
 CC deduced amino acid sequences (see AAY58454-57). It also provides methods
 CC of using the gene and cDNA sequences to produce genetically engineered
 CC *Populus* species and other trees having modified fertility
 CC characteristics, including sterility. Genetic constructs useful in
 CC producing genetically engineered *Populus* and other trees include
 CC antisense versions of PTD, dominant negative mutants, and constructs
 CC useful for sense suppression. Promoter sequences may be used to obtain
 CC floral specific expression of genes such as cytochrome P450 genes
 CC in genetic ablation strategies to produce trees having modified fertility
 CC characteristics, including sterility. Sterile trees allow increased wood
 CC yield and a reduction in the production of allergens such as pollen
 CC
 XX SQ Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,676-66 Length: 924
 Score: 701.50 Matches: 147
 Percent Similarity: 72.38% Conservative: 26
 Best Local Similarity: 61.51% Mismatches: 45
 Query Match: 57.69% Indels: 21
 DB: 3 Gaps: 5

US-10-069-527-4 (1-232) x AA257943 (1-924)

QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 DB 1 ATGGGTCGTGGAAGATGAAATCAAGAAAGATGAAACCCCAAAACGGCAAGTCAC 60
 QY 21 TysSerLysArgArgAsnGlyIlePheLysValAlaGlnGluLeuThrValLeuCysAsp 40
 DB 61 TACTCGAAGAGAAAGATGATTTTCAAGAAAGCCCAAGACTCTGCTGCTTGTGAT 120
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnTyrIleSerPro 60
 DB 121 GCTAAGGTCTCTTATCATCTGTCCTCCCAACATCAACAACTCAATGATGATTAACCCC 180
 QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
 DB 181 TCCACATCGAAGAAAGATCTACGATCAATATCAAGCAAGCTTTAGCAATGATCTGTG 240
 QY 81 ArgThrHisGlnLysSerMetLysAspThrLeuTyrLysLeuLysGlnIleAsnLys 100
 DB 241 GGCACCTCAATACGAGAAATGCAAGACCTTGAAGAGACTGATGATATCATCATTAAG 300

QY 101 LeuArgArgGluIleArgGlnAArgGlnLysAspLeuAsnArgLysLeuSerPheAspLeu 120
 DB 301 CTGAGACAGAAATAGGACAG 360
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerLeuAspAlaIleArgGlnArgLysTyr 140
 DB 361 CTGCGCGGTCTTGACCAACATATGATGACCTGATGATGATGATGATGATGATGATGAT 420
 QY 141 HisValIleLysThrGlnThrGluThrThrLysLysLysValLysAsnLeuGlnArg 160
 DB 421 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 161 ArgGlnAsnMetLeuHisGlyTyrPheAspGlnGluAlaAlaGlyGluAspProGlnTyr 180
 DB 481 CATGATAAAGCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
 QY 181 GlyTyrGluAspAsnGluGlyLysAspTyrGlnSerLysLeuAlaLeuSerAsnGlyAlaAsn 200
 DB 532 GATTAGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
 QY 201 AsnLeuTyrThrPheHisLeuHisHisHisHisHisHisHisHisHisHisHisHis 212
 DB 580 AACCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 639
 QY 213 HisHisGlyGlySerSerLeuGlySerSerLeuThrHisLeuHisAspLeuArgLeu 231
 DB 640 CACCTT---GGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 678
 RESULT 7
 ID AA051189 standard; DNA; 882 BP.
 XX
 XX AA051189;
 AC 25-MAR-2003 (revised)
 DT 19-JUN-1994 (first entry)
 XX
 XX Homeotic gene green petal.
 XX
 XX Plant; organ morphogenesis; control; petunia; petals; ss.
 XX
 OS Petunia.
 XX
 FH Key location/Qualifiers
 FT CDS 17..713
 FT /tag=a
 PN WO9321322-A1.
 XX
 XX 28-OCT-1993.
 PD
 XX 13-APR-1993; 93WO-US003508.
 PF
 XX 13-APR-1992; 92US-00867580.
 PR 06-JUL-1992; 92US-00909589.
 XX
 PA (UNIV OREGON HEALTH SCI.
 PI Halford U, Van Der Krol AR, Kush A, Chua N;
 DR WPI; 1993-351732/44.
 DR P-PSDB; AAR43385.
 XX
 PT Plant organ morphogenesis control and determ. - by regulating the
 PT expression of homeotic genes which determine the identity of the organ.
 XX
 PS Claim 13; Fig 2; 74pp; English.
 CC The homeotic gene green petal from petunia has been cloned and
 CC characterised previously. The gene was used in a new method for
 CC controlling the morphogenesis of plant organs comprising regulating the
 CC expression of the gene using ectopic expression. Such a method can be

CC used to determine and control plant organ morphogenesis, such as
 CC modifying petals without altering the reproductive portions of the
 CC flower. See also A0501190-1. (updated on 25-MAR-2003 to correct PN
 CC field.)

SQ Sequence 882 BP, 306 A, 155 C, 182 G, 239 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	1-056-59	Length:	882
Score:	641.50	Matches:	129
Percent Similarity:	71.12%	Conservative:	36
Best Local Similarity:	55.60%	Mismatches:	52
Query Match:	52.75%	Indels:	15
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US-10-069-527-4 (1-232) x A0501189 (1-882)

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QY 21 TTTCTTAAGAGAAAGAAATGCACTTTTCAAGAAAGCTAATGCACTCTTCTTGTGAT 40
DB 78 TTTCTTAAGAGAAAGAAATGCACTTTTCAAGAAAGCTAATGCACTCTTCTTGTGAT 137
QY 41 AlAlaValSerLeuIleMetLeuSerAsnThrAsnIleMetLeuIleGluTyrIleSerPro 60
DB 138 GCCAAGATTCATATTAATGATTTCCAGTCTGCAAGCTTCAAGATTCATATTAATGATTC 197
QY 61 ThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 80
DB 198 TTTATCAGACATGAGAGATGTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 257
QY 81 ArgThrHisGluGluSerMetLeuSerAsnThrThrThrThrThrThrThrThrThrThr 100
DB 258 AACCTCCCATATGAGAAATGCAAGAGCACTGAGAAAGCTTAAGAAAGTAAATGCAAT 317
QY 101 LeuAlaArgGlnIleArgGlnIleArgGlnIleHisAsnLeuAsnGlyLeuSerPheAsp 120
DB 318 CTCCTCAAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAG 377
QY 121 LeuAlaSerLeuAspArgIleMetGlnSerSerLeuAspArgAlaIleArgGlnArgIle 140
DB 378 TTGGAAGAGCTATGAGAAATGTCACATCTCTCAAGCTTATTCGTAAGAAAGATAT 437
QY 141 HisValIleLeuThrGlnIleThrGlnIleThrGlnIleValValValValValValVal 160
DB 438 AAGGATGATGCAATCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 497
QY 161 ArgGlyAsnMetLeuHisGlyTyrPheArgGlnIleAlaGlyGluAspProGlnIle 180
DB 498 CATAGGATCTCTG-----CTTGAATTTAGCAAGCAAGAGAGAGAGAGAGAGAGAG 545
QY 181 GlyTyrGluAspArgGlnIleGluIleGluIleGluIleGluIleGluIleGluIleGlu 200
DB 546 GGGCTAGAGTGAACAGAGAGTGAACATCTGAGCTTGTTCCTCAAGTGAAGAGAGAG 605
QY 201 AsnLeuTyrThrPheHisLeu-----HisHisProAsnLeu 212
DB 606 GGCATATTAAGCTTAAGCTTCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 665
QY 213 HisHisGlyGlySerSerLeuGlySerSerIleThr 224
DB 666 CACAGAGGTGGA-----GGCTCTGATATCACT 692

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RESULT 8
 AAD42259 standard; cDNA, 926 BP.
 AAD42259;
 AAD42259;
 04-NOV-2002 (first entry)

DE Soybean AP3 homologue cDNA from clone sflin.pk001.116.

XX Floral developmental protein; flowering locus T; APTFLA3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW sterility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; soybean; gene; ss.

XX Glycine max.

OS Location/Qualifiers

FT Key 11.694

FT CDS /tag= a /product= "Soybean AP3 homologue protein"

XX W0200244390-A2.

XX 06-JUN-2002.

XX 21-NOV-2001, 2001WO-US043750.

XX 28-NOV-2000, 2000US-0253415P.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
 DR WPI; 2002-547703/58.

XX P-PSDB; AAE25757.

XX New floral developmental polypeptide having flowering locus T or AP3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.

XX Claim 6; Page 80; 88pp; English.

XX The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APTFLA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or TFL homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is soybean AP3 homologue
 CC cDNA

XX SQ Sequence 926 BP, 304 A, 195 C, 194 G, 233 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	5-626-57	Length:	926
Score:	616.50	Matches:	118
Percent Similarity:	70.35%	Conservative:	41
Best Local Similarity:	52.21%	Mismatches:	60
Query Match:	50.70%	Indels:	7
DB:	6	Gaps:	3

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QY 1 MetAlaArgGlyLeuIleGluIleLeuIleGluAlaGlnIleThrAsnArgGlnValThr 20
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QY 21 TTTCTTAAGAGAAAGAAATGCACTTTTCAAGAAAGCTAATGCACTCTTCTTGTGAT 40
DB 71 TACTCTAAACGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 130
QY 41 AlAlaValSerLeuIleMetLeuSerAsnThrAsnIleMetLeuIleGluTyrIleSerPro 60

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Db      607 GCCGCCGCCGCTGCTTGTACACCTCGCCGCAACCGACGACCCCAATCTTACTAGC 666
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RESULT 10
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ID      AAC40831 standard; DNA; 959 BP.
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AC      AAC40831;
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DT      17-OCT-2000 (first entry)
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DE      Arabidopsis thaliana DNA fragment SEQ ID NO: 29696.
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KM      Hybridisation assay; genetic mapping; gene expression control;
KM      protein identification; signal transduction pathway; metabolic pathway;
KM      promoter; termination sequence; ss.
XX
OS      Arabidopsis thaliana.
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PN      EP1033405-A2.
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PD      06-SEP-2000.
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PF      25-FEB-2000; 2000EP-00301439.
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Alignment Scores:

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US-10-069-527-4 (1-232) x AAC40831 (1-959)

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 DB 564 GCACTAGTACAAATGAGGAGATTAACACTCACTTCTGGATTCAAATCGAAGGTCAT 623
 QY 201 AsnLeuTyrThrPheHisLeuHisHisProAsnLeuHis 214
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RESULT 11
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 AC AAC51525;
 DT 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68842.
 XX Hybridisation assay; genetic mapping; gene expression control;
 KM protein identification; signal transduction pathway; metabolic pathway;
 XX promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 PF 25-FEB-2000; 2000EP-00301439.
 XX 25-FEB-1999; 99US-0121825P.
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 QY 21 TySerIysArgArgAsnGlyIlePheIleIysAlaGlnGluLeuThrValLeuCyAsp 40
 Db 313 TATTCAAGAGAGAAATGCTTATTATTCAGAAACACATGAGCTCAGCGTTTCTGAT 372
 QY 41 AlAluValSerIleuIleMetLeuSerAsnThrAsnIleuMetIleGlyIleSerPro 60
 Db 373 GCTAGGCTTTCATATCATGTTCTCTCAGCCACAGCTTCATGAGATATCAGGCTT 432
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 QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
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 QY 141 HisValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 160
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 QY 161 ArgGlyAsnMetLeuHisGlyIlePheAspGlnGluIleAlaGlyIleAspProGlnIleTyr 180
 Db 733 CAAGAAGATCTCATACAT-----GAGCTGGAATAGAGCTGAGAGATCTCTACTAT 783
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 Db 784 GGACTAGTACAGATGAGAGGATGATGACTCAGTTCTGATGATCAACAAATGAGAGGTCA 843
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 AC AAD42257;
 XX
 DT 04-NOV-2002 (first entry)
 XX
 DE Corn AP3 homologue cDNA from clone ctain.PK050.48.
 XX
 KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW sterility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; corn; gene; ss.
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
 FT CDS 131..814
 FT /*tag= a
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 W0200244390-A2.
 XX
 PD 06-JUN-2002.

PF 21-NOV-2001; 2001WO-US043750.
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 PR 28-NOV-2000; 2000US-0253415P.
 XX
 PA (DUP0) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
 DR MPI: 2002-547703/58.
 DR P-PSDB; AAE25755.
 PT New floral developmental polypeptide having flowering locus T or Ap3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.
 PS Claim 6, Page 77-78; 88pp; English.
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or TFL homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is corn AP3 homologue cDNA
 XX
 SQ Sequence 1257 BP; 320 A; 353 C; 340 G; 244 T; 0 U; 0 Other;
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 QY 41 AlAluValSerIleuIleMetLeuSerAsnThrAsnIleuMetIleGlyIleSerPro 60
 Db 251 GCCAGGTCGCGCATCATATGTTCTCTCCACCGGCAAGTACACAGCTCTGACAGCCCC 310
 QY 61 ThrThrThrIleSerMetIleAspAspIleGlnIleThrMetGlyIleAspLeuTrp 80
 Db 311 GGAACGACATCAAGACCATTTGACCGTACCAAGAGCCATCGGACCAAGCTATGG 370
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 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgIleTyr 140
 Db 491 CTGGCGGCTCTCAGACAAAGCTGACGCGGCTCTCAAGAGAGGTCCCATAGAGATAC 550

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 05:39:13 ; Search time 72.1432 Seconds
(without alignments)
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Title: US-10-069-527-4

Perfect score: 1216

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Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	709.5	58.3	946	4	US-09-410-464-2
3	419.5	34.5	4285	4	US-09-410-464-1
4	296	24.3	945	2	US-08-485-981-9
5	296	24.3	945	2	US-08-867-087B-10
6	295	24.3	1059	2	US-08-867-087B-14
7	287	23.6	1180	2	US-08-867-087B-16
8	285	23.4	798	4	US-09-611-659A-3
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13	280	23.0	1062	3	US-09-349-677-1	Sequence 1, Appli
14	280	23.0	1062	4	US-09-708-584-1	Sequence 1, Appli
15	279	22.9	959	3	US-09-067-800-7	Sequence 7, Appli
16	279	22.9	959	3	US-09-349-677-7	Sequence 7, Appli
17	276	22.7	1070	3	US-08-904-284-1	Sequence 1, Appli
18	276	22.7	1141	2	US-08-323-449B-1	Sequence 1, Appli
19	276	22.7	1141	2	US-08-485-981-1	Sequence 1, Appli
20	276	22.7	1141	2	US-08-867-087B-1	Sequence 1, Appli
21	273.5	22.5	1257	4	US-09-433-579-1	Sequence 1, Appli
22	271	22.3	1345	1	US-08-592-214A-7	Sequence 7, Appli
23	271	22.3	1345	1	US-08-592-214A-7	Sequence 7, Appli
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40	263.5	21.7	779	3	US-08-555-227-9	Sequence 9, Appli
41	263.5	21.7	779	3	US-08-555-227-9	Sequence 9, Appli
42	263.5	21.7	779	3	US-09-149-976-9	Sequence 9, Appli
43	263.5	21.7	794	4	US-09-398-326-9	Sequence 9, Appli
44	262.5	21.6	794	4	US-08-592-214A-3	Sequence 3, Appli
45	262.5	21.6	794	3	US-08-559-188-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-410-464-3
Sequence 3, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 681
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(681)
US-09-410-464-3

Alignment Scores:
Pred. No.: 8.65e-79
Score: 709.50
Percent Similarity: 72.38%
Best local Similarity: 62.34%
Query Match: 58.35%
DB: 4
Gaps: 5
US-10-069-527-4 (1-232) x US-09-410-464-3 (1-681)

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Qy      1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
Db      1 ATGGGTGCTGGAAGATTGAATCAAGAGATCGAAATCCCAACAAACAGGCAAGTACC 60
Qy      21 TySerLysArgAspGlnGlyIlePheLysValIleGlnGluLeuThrValLeuCysAsp 40
Db      21 TACTCGAAGAGAAATGATATTTTCAAGAAACCCCAAGAACTCACTGACTTGTGAT 120
Qy      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluIleThrIleSerPro 60
Db      121 GCTAAGTCTCTCTTATCAATGTTCTTCAACACTACAACTCAATGAGTCAATTAAGCC 180
Qy      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
Db      181 TCCACATCGACAAAGAGATCTCAATCAATATCAAGAACCTTTAGGCAATAGATCTGTGG 240
Qy      81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnLys 100
Db      241 GGCACTCAATTCGGAAGAAATGCAAGACACTTGGAGAGCTGAATGATATCAATCAATAG 300
Qy      101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db      301 CTGAGACAGAAATCAAGCAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360
Qy      121 LeuAlaSerLeuAspAspGlnMetGlnSerSerLeuAspAlaIleArgGlnArgTyr 140
Db      361 CTGGCGGCTCTTGGAACAATATGACTGAAGCCTTGATGTGTGCTGGCAGAAATGAC 420
Qy      141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArgTyr 160
Db      421 CATGTGATCAAAACAAACAAAGAACTTACAGAGAGAGAGAGAGAGATTTAGAGAGAGA 480
Qy      161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyGluAspProGlnTyr 180
Db      481 CATGAAACCTCTTGATGAGAAATAT-----GAGCAAAACTAGAGATTCACAGTAT 531
Qy      181 GlyTyrGluAspAsnGlnGlyAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
Db      532 GCTTAGTGACAAAT-----GAGCTGCTGTTGCACTTGCAAATGGGCTTCC 579
Qy      201 AsnLeuTyrThrPheHisLeuHis-----ProAsnLeu 212
Db      580 AACCTCTATGCATTCGCCCTGCATCAAGGACACACACACACCATCTCCCTATCTT 639
Qy      213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231
Db      640 CACCTT---GGAAGATGATTTGGAGCC-----CATGAACCTTCCGCTT 678

RESULT 2
US-09-410-464-2
; Sequence 2, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentia Ver. 2.0
; SEQ ID NO 2
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
US-09-410-464-2

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Alignment Scores:
Pred. No.: 1,426-78
Score: 709.50
Percent Similarity: 72.38%
Best Local Similarity: 62.34%
Query Match: 58.35%
DB: 4 Gaps: 5

US-10-069-527-4 (1-232) x US-09-410-464-2 (1-946)

Qy      1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
Db      1 ATGGGTGCTGGAAGATTGAATCAAGAGATCGAAATCCCAACAAACAGGCAAGTACC 60
Qy      21 TySerLysArgAspGlnGlyIlePheLysValIleGlnGluLeuThrValLeuCysAsp 40
Db      21 TACTCGAAGAGAAATGATATTTTCAAGAAACCCCAAGAACTCACTGACTTGTGAT 120
Qy      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluIleThrIleSerPro 60
Db      121 GCTAAGTCTCTCTTATCAATGTTCTTCAACACTACAACTCAATGAGTCAATTAAGCC 180
Qy      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
Db      181 TCCACATCGACAAAGAGATCTCAATCAATATCAAGAACCTTTAGGCAATAGATCTGTGG 240
Qy      81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnLys 100
Db      241 GGCACTCAATTCGGAAGAAATGCAAGACACTTGGAGAGAGAGAGAGAGATTTAGAGAGAGA 300
Qy      101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db      301 CTGAGACAGAAATCAAGCAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360
Qy      121 LeuAlaSerLeuAspAspGlnMetGlnSerSerLeuAspAlaIleArgGlnArgTyr 140
Db      361 CTGGCGGCTCTTGGAACAATATGACTGAAGCCTTGATGTGTGCTGGCAGAAATGAC 420
Qy      141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArgTyr 160
Db      421 CATGTGATCAAAACAAACAAAGAACTTACAGAGAGAGAGAGAGAGATTTAGAGAGAGA 480
Qy      161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyGluAspProGlnTyr 180
Db      481 CATGAAACCTCTTGATGAGAAATAT-----GAGCAAAACTAGAGATTCACAGTAT 531
Qy      181 GlyTyrGluAspAsnGlnGlyAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
Db      532 GCTTAGTGACAAAT-----GAGCTGCTGTTGCACTTGCAAATGGGCTTCC 579
Qy      201 AsnLeuTyrThrPheHisLeuHis-----ProAsnLeu 212
Db      580 AACCTCTATGCATTCGCCCTGCATCAAGGACACACACACACCATCTCCCTATCTT 639
Qy      213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231
Db      640 CACCTT---GGAAGATGATTTGGAGCC-----CATGAACCTTCCGCTT 678

RESULT 3
US-09-410-464-1
; Sequence 1, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851

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EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 4285
TYPE: DNA
ORGANISM: *Populus balsamifera* subsp. *trichocarpa*
US-09-410-464-1

Alignment Scores:
Pred. No.: 1.37e-41 Length: 4285
Score: 419.50 Matches: 150
Percent Similarity: 29.26% Conservative: 25
Best Local Similarity: 25.08% Mismatches: 46
Query Match: 34.50% Indels: 379
DB: 4 Gaps: 12

US-10-069-527-4 (1-232) x US-09-410-464-1 (1-4285)

QY 1 MetAlaArgGlyLeuIleGluIleLeuSerLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 2001 ATGGGTGCGTGAAGATTGTAATCAAGAGATCGAAAGCCACAGAAACAGGAGATCACC 2060

QY 21 TyrSerLeuArgArgAsnGlyIlePheIleValAlaGlnGluLeuThrValLeuCysAsp 40
DB 2061 TACTCGAAGAGAGAAATGTAATTTTCAAGAAAGCCCAAGAACTCATCTGACTTGTGAT 2120

QY 41 AlaIysValSerLeuIleMetLeuSerAsnThrAsnLeuMetLeuGluTyrIleSerPro 60
DB 2121 GCTAAGCTCTCTTATCATGTTCTTCCAACTAACAACCAATCAAGATACATTAGCCCC 2180

QY 61 ThrThrThr----- 63
DB 2181 TCCACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2240

QY 63 ----- 63
DB 2241 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2300

QY 64 -----ThrIysSerMetTyrAspTyrGlnIleVal 74
DB 2301 GATGTTTATTTGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2360

QY 74 MetGlyIleAspLeuIlePheIleValAlaGlnGluLeuThrValLeuCysAsp 85
DB 2361 TTTAGGCAATGATCTGTGGGCACTCAATACAGAGTTAACTTCTTCTTCTTCTTCTTCTT 2420

QY 85 ----- 85
DB 2421 CTAATGTTTGAATCTATGAGCAATATGATGATGATGATGATGATGATGATGATGATGATG 2480

QY 86 -----SerMetIysAspThrLeuIlePheIleValAlaGlnGluLeuThrValLeuCysAsp 104
DB 2481 GCAGAAATATGCAAGACACTTGAAGAGCTGATGATGATGATGATGATGATGATGATGATG 2540

QY 104 uile----- 105
DB 2541 AATTCAGTACTTCAAAAGAAATAACCTTCGATATGATGATGATGATGATGATGATGATG 2600

QY 106 -----ArgGlnArgL 109
DB 2601 GGAATATCTGTAATTTTGGAGCTACTATTAAGTATTTGTTTAAAGGCGAGAGGA 2660

QY 109 euGlyHisAspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspAspGluMetG 129
DB 2661 GAGGAGAGGCGCTGATGATCTGAGCATTTGATCATCTGCGCGCTTGAACAACATATGA 2720

QY 129 InsSerLeuAspAlaIleArgGlnArgLys----- 139
DB 2721 CTGAGGCTTGAATGATGCTGCTGCGAGGAA-GGTGATGATGTTTCAAGTGAACATCTTT 2779

QY 139 ----- 139

DB 2780 ATATTAATTCAGATTTCTAATTCCTAAATTTGAGCTACTAGTAAATTGAGTTCGCTCC 2839

QY 139 ----- 139

DB 2840 GGTGTATCAAGCAGGTTAATCTAGATCTGATTTTCTTCTTCAAAATCAAGTCAATT 2899

QY 139 ----- 139

DB 2900 TGAATTTTAAATAAAAAATATGATTTTGAATCAACTATACAAATATCATCATC 2959

QY 139 ----- 139

DB 2960 ACAATCGAATCTTACATTTATCAAACTTCAAAATAGATCTTATTAATATGATATA 3019

QY 139 ----- 139

DB 3020 CCGGTGCTTTTATGAT 3079

QY 139 ----- 139

DB 3080 TTTTAAATTTGATTTATTTATCTTATCAATTTTATCATTTTGGGATTTGAA 3139

QY 139 ----- 139

DB 3140 ACCGTGTTAGAAAGAAATATACACACCTTGAACCTTGCTTTTACCTTGCATTAAG 3199

QY 139 ----- 139

DB 3200 GATTTTCATGATGATTTTGGGTAAACCTTAACCTCATATAGAGGATATGCTT 3259

QY 140 -----TyrHisValI 143

DB 3260 GTAATTAACACTTACACTTACAGTTCAACATCTTGTATTTATTAACATGATGATG 3319

QY 143 IeIysThrGlnThrGluThrThrIleIysIleIys----- 153

DB 3320 TCAAAACCAAAAGAAACCTTACAGAGAGAGTTGATATAAAGAACATTTTACCTC 3379

QY 154 -----ValIleVal 156

DB 3380 TTCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3439

QY 156 snIeuGluGlnArgArgGlyAsnMetLeu----- 165

DB 3440 ATTTAGAGAGAGCATGAGAACTCTTGTATGAAATATGTAACAACTTAATTTTCATGT 3499

QY 166 -----HisGly-----TyrP 169

DB 3500 GCTTGTTCGTAAATTTTCCAACTTGAAACACATGATTAATACTGAGATTTT 3559

QY 169 heAspGlnGluAlaIleGly-----GluAspProGlnIleTyrGly 183

DB 3560 TTTCTTTTGT-GCTTGGGATTTTAAGAGCAAACTAGAGGATTCACAGTATGTTTAG 3618

QY 183 IuAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsnAsnLeu 203

DB 3619 TGAGCAT-----GAGAGCTGCTTGCATCTGCAAAATGGGGCTTCCAACTCT 3666

QY 203 yThrPheHisLeuHisHis-----ProAsnLeuHisHisG 215

DB 3667 ATGCATTCGCGCTGATCAAGGAGCAACACACACACATCTCCCTTAATCTTCACTT 3725

QY 215 IyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231

DB 3726 --GAGATGATTTGAGGCC-----CATGACCTTCGCTT 3758

RESULT 4
US-08-485-981-9
Sequence 9, Application US/08485981
Patent No. 5861542
GENERAL INFORMATION:
APPLICANT: An. Gynheung
TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND

TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klarquist Sparkman Campbell Leigh &
 ADDRESSEE: Whinston
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 STREET: Suite 1600
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,981
 FILING DATE: June 7, 1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/323,449
 FILING DATE: October 14, 1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan. E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-42933
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 945 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 US-08-485-981-9

Alignment Scores:
 Pred. No.: 3,04e-27 Length: 945
 Score: 296.00 Matches: 77
 Percent Similarity: 53.33% Conservative: 35
 Best Local Similarity: 36.67% Mismatches: 68
 Query Match: 24.34% Indels: 30
 Gaps: 6

US-10-069-527-4 (1-232) x US-08-485-981-9 (1-945)

QY 1 Metlaargtlylsilegllulelyleuileglsnolntrhsenatrginvalntr 20
 Db 16 ATGGGAAGGGGTAGGGTGTAGCTTAAAGAAATAGAGAACAGATCAACAGCAAGTGAAC 75
 QY 21 Tyserlysatgataaganglyilephelylsysalaglngluleuthrvalleucysasp 40
 Db 76 TTCCCTAAGAGAAATGACCTTTGAAAAAGCTTATAGCTTTCTGTTCTTTGTGAT 135
 QY 41 Alalyvalserleuilemetleuserasntrhsnlysmethisgluyrileserpro 60
 Db 136 GCTAGAGTGTCTCATCATCTTCTCCAAATAGGGGAAACGTACAGGTTCTCAGTAGC 195
 QY 61 Thtrhrthrlyssermetlyraspapyrlylulys-----Thr 74
 Db 196 TCTAGCATGCTCAAGACATTA--GAGAGGTACCAAGAGTCAACAGATATCTTGAGCTT 252
 QY 75 Metglyleaspleutratpgrthhsiglulusermetlysaapthrlleutplysleu 94
 Db 253 ACCAATATATCCACAGACAGACCTGGAATAATAGTCAACAGATATCTTGAGCTT 312
 QY 95 lyeagluleasnaulysleuargarglulilearglirglenclylhsaapleuaen 114
 Db 313 AAAGCAGCTTACGAGACGATTAACAGCATCAAGAGAAATCTTCTGTGAGAAATCTTGCG 372

QY 115 GlyleuserpneaspGluLeuAlaserleuaspasglumetGlnserSerleuaspAla 134
 Db 373 CTTTATATAGCAAGAACTTGAATCACTTATAGAGGAGCTTGAATATGTCACTGAAACAG 432
 QY 135 ilearg-----Glnarglystyr 140
 Db 433 ATTCAATCACTCGGACTCACTTATATGTGATCACTTACAGATCTTCAAGAAAGGAA 492
 QY 141 Hisvalilleysthrlthrlthrlthrlthrlthrlthrlthrlthrlthrlthrlth 160
 Db 493 CATGCAATTAAAGAAAGCAAGCAACCTTGAACAAAGCTTG-----ATG 537
 QY 161 ArgglyanmetleuilegltlyrphesapnglnglualalaglyluaspProglntyr 180
 Db 538 GAAGAGAGCAACTTAATCTGACGTGGCAACAAATGCA-----CAAGATATGGGCTAC 591
 QY 181 GlyTYrglu-----AspAsnGluGlyasp 188
 Db 592 GGCGGCAAAACAATCAATCAAGGGCGAT 621

RESULT 5
 US-08-867-087B-10
 Sequence 10, Application US/08867087B
 Patent No. 5990386
 GENERAL INFORMATION:
 APPLICANT: An. Gynheung
 TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klarquist Sparkman Campbell Leigh &
 ADDRESSEE: Whinston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 STREET: Suite 1600
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/867,087B
 FILING DATE: June 2, 1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/323,449
 FILING DATE: October 14, 1994
 APPLICATION NUMBER: U.S. 08/485,981
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan. E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-47071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 945 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 US-08-867-087B-10

Alignment Scores:
 Pred. No.: 3,04e-27 Length: 945
 Score: 296.00 Matches: 77
 Percent Similarity: 53.33% Conservative: 35

Best Local Similarity: 36.67% Mismatches: 68
 Query Match: 24.34% Indels: 30
 DB: 2 Gaps: 6

US-10-069-527-4 (1-232) x US-08-867-087B-10 (1-945)

QY 1 MetAlaArgGlyLysIleGluIleuLeuIleGluAsnGlnThrAsnArgIleValThr 20
 DB 16 ATGGAGAGGGTGAAGGTTGAGCTTGAAGATAGAGAACAGATCAACAGGCAAGTAC 75
 QY 21 TyrSerLysArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
 DB 76 TTCGCTAAGAGAGAAATGAGACTTTGAAAAAGCTTAGAGCTTTCGTTCTTGTCAT 135
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHsGluTyrIleSerPro 60
 DB 136 GCTGAGGTTGCTCATCATCTTCTCAATAGGGGAAAACTGACAGAGTCTGACAGTAC 195
 QY 61 ThrThrThrThrLysSerMetLysAspAspTyrGlnLys-----Thr 74
 DB 196 TCTACAGCTCTCAAGACATTA---GAGAGGTACCAAGAGTGCACACTACGACACAGAG 252
 QY 75 MetGlyIleAspLeuTyrPheThrHsGluGlnSerMetLysAspThrLeuTyrLysLeu 94
 DB 253 ACCAATATATTCACACAGAGAGCACTGGAAATATAGTACCAACAGAAATACCTGAGCTT 312
 QY 95 LysGluIleAsnAsnLysLeuArgArgIleAlaArgIleGlnArgLysIleAsn 114
 DB 313 AAAGACGTTACGAGCACTTACAGGATCACAGAGAAATCTTCTTGAAGATCTTGAC 372
 QY 115 GlyLeuSerPheAspGluLeuAlaSerLeuAspAspGlnLeuSerSerLeuAspAla 134
 DB 373 CCTTGATAGCAAGAACTTGAATCACTTGAAGAGCACTTGATATGCTGAGAAAG 432
 QY 135 IleArg-----GlnArgLysTyr 140
 DB 433 ATTCATCACTACGAGCTCACTGAATGTTGATCACTTACAGATCTTCAAGAGAAAGAA 492
 QY 141 HsValIleLysThrGlnThrGlnThrLysLysValLysValLysAsnLeuGlnArg 160
 DB 493 CATGCACTTAACGAGAAACAGAACTTGAACAAAGCTG-----ATG 537
 QY 161 ArgGlyAsnMetLeuHsIleGlyTyrPheAspGlnGlnAlaAlaGlyAspProGlnTyr 180
 DB 538 GAAGAGAGCACTAATCTGACAGTGGCAACAAATGCA-----CAAGATATGGGCTAC 591
 QY 181 GlyTyrGlu-----AspAsnGluLysAsp 188
 DB 592 GGCCGGCAAACTCAAACTCAGGGCGCAT 621

RESULT 6
 US-08-867-087B-14
 Sequence 14, Application US/08867087B
 Patent No. 5990386
 GENERAL INFORMATION:
 APPLICANT: Am. Gynheung
 TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
 TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klarquist Sparkman Campbell Leigh &
 ADDRESSEE: Winston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/867,087B
 FILING DATE: June 2, 1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/323,449
 FILING DATE: October 14, 1994
 APPLICATION NUMBER: U.S. 08/485,981
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan, E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1059 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 US-08-867-087B-14

Alignment Scores:
 Pred. No.: 4,8e-27 Length: 1059
 Score: 295.00 Matches: 83
 Percent Similarity: 49.40% Conservative: 41
 Best Local Similarity: 33.07% Mismatches: 71
 Query Match: 24.26% Indels: 56
 DB: 2 Gaps: 9
 US-10-069-527-4 (1-232) x US-08-867-087B-14 (1-1059)

QY 1 MetAlaArgGlyLysIleGluIleuLeuIleGluAsnGlnThrAsnArgIleValThr 20
 DB 98 ATGGAGAGGGGCGGGGAGCTGAAGAGATGAGAAACAGATCAACCGAAGGTGACG 157
 QY 21 TyrSerLysArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
 DB 158 TTCGCCAAGAGAGAAATGAGCTCTCTCAAGAGCGGTACAGAGCTTCCGCTCTGGAC 217
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHsGluTyrIleSerPro 60
 DB 218 GCGAGGTCGCTCATCATCTTCTCAACCGCGGCAAGCTTACGAGTCTGACAGACC 277
 QY 61 ThrThrThrThrLysSerMetLysAspAspTyrGlnLysThr-----MetGlyIleAsp 78
 DB 278 CAGAGCATGACTTAACGCTT---GAGAGATCAAGAAATGCACTTACGAGAGACCCGAA 334
 QY 79 LeuTyrPheThrHsGluGlnSer-----MetLysAspThrLeuTyrLys 93
 DB 335 ACAGCTCCAAATATAGAGAAATGAGCAATGAAAGCTAGCCGATGATGACTCAAA 394
 QY 94 LeuLysGluIleAsnAsnLysLeuArgArgGluIleArgGlnArgLysIleAspLeu 113
 DB 395 CTGAAGAGCAAGGTTGAAATTTACACAGGACTCAAGAAATTTGCTGGGTTCAGATCTT 454
 QY 114 AsnGlyLeuSerPheAspGluLeuAlaSerLeuAspAspGlnLeuSerSerLeuAsp 133
 DB 455 GATTCATTAGGCAATTAAGAGCTGAGAGCTTAGAGAGAGAGCTGATTATCCCTGAAG 514
 QY 134 AlaIleArg-----GlnArgLys 139
 DB 515 CACGTCAGAACTACAGAGCAAAACATCTGTGACCACTGACGAGCTTCAAGAGAAAG 574
 QY 140 TyrHsValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGln 159
 DB 575 GAACAAATGTTTGTGAAGCAAAATGATGCTTACGAGAAATCTGAGAGAAAGACAT 634
 QY 160 ArgArgGlyAsnMet----- 164

Db 635 GTTCGGGAGCAGAGTGTGGAGCAGGCTGCAACTTAATGGCTATGACCTGACGCT 694
Qy 165 -----LeuH:sgly-----TyrPheaspGlnGluAlaIaGly 175
Db 695 GAATGACGACAGCCCTTTCACGGCGGCAATGGCTTTCATCCATGATGCTGCTGCT 754
Qy 176 GluaspPro---GlnTyrGlyTyr-----GluaspGlnGluaspTyrGluSerAla 192
Db 755 GAACCCACCCCTTCATGATGGGTACCGTCAGACGATCATGAG-----796
Qy 193 LeuAlaLeuSeraspGlnGluAlaaspLeuTyr 203
Db 797 ---GGATGAACAGTGGCTGATGAACACCTAC 826
RESULT 7
US-08-867-087B-16
; Sequence 16, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: At, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kiarquist Sparkman Campbell Leigh &
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867, 087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-867-087B-16
Alignment Scores:
Pred. No.: 5.56e-26 Length: 1180
Score: 287.00 Matches: 76
Percent Similarity: 55.72% Conservative: 36
Best Local Similarity: 37.81% Mismatches: 65
Query Match: 23.60% Indels: 24
DB: 2 Gaps: 7
US-10-069-527-4 (1-232) x US-08-867-087B-16 (1-1180)
Qy 1 MetAlaargGlyLysIleGlnIleLysLeuIleGluAsnGlnThrAspArgGlnValThr 20

Db 110 ATGGGAGAGGAGGAGGTGGAGCTGAAGAGATCGAAGAACAGATGACAGGAGGTGAC 169
Qy 21 TyrSerLysArgAlaAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCyasp 40
Db 170 TTGGCGAAGCGGAGGAATGGGCTGCTCAAGAGGGGTGACAGCTCTCCGTGCTGCGAC 229
Qy 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlyTyrIleSerPro 60
Db 230 GCGAGGTGCGCCCTATCATCTTCTCCACCGCGGCAAGCTCTAGCATTTCTGACGCGG 289
Qy 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMet-----GlyIleasp 78
Db 290 CAAGCATGACCCAGAACTTTG---GAAAGATACCAAAATTCAGTTATGTGGGCGCAGAT 346
Qy 79 LeuTPrArgThrHisGluGlu-----SerMetLysAspThrLeuTPrLys 93
Db 347 ACTGCAATACAGAAACAGAAATATGATGATGCAAGACCGCAATGATGACTCTCAA 406
Qy 94 LeuLysGlnIleAsnAsnLysLeuArgArgGlnIleArgGlnArgLeuGlyHisAspLeu 113
Db 407 CTGAAGCAGCGGCTGGAATAATTACAGAGACCCAAAGGATCTTCTTGAGAGATCTT 466
Qy 114 AsnGlyLysSerPheaspGlnLeuAlaSerLeuAspArgLysMetGlnSerSerLeuasp 133
Db 467 GGGACACTTGGCATMAAAGAGCTAGAGCAGCTTGAGAAACACTTGATTCCTTGAGG 526
Qy 134 AlaIleArgGln---ArgLysThrHisValIleLysThrGlnThrGlnThrThrLysLys 152
Db 527 CACATTAGATCCACAGAGACACAGCATATGCTTGATGACGTGATGATCTCCAGAGAGG 586
Qy 153 LysVal-----LysAsnLeuGlnGlnArgArgGly 162
Db 587 GAACAAATGTGTGTGAAGCAATTAAGTCTCAGAAAGAAACCTGGAGAG-----AGC 640
Qy 163 AsnMetLeuHisGlyTyrPheaspGlnGluAlaIleGlyLysAspProGlnTyrGlyTyr 182
Db 641 AACCACTTGATGACAGCAAGCTGGAGAGACCGGCC-----ACCACTGCGCTAC 691
Qy 183 Glu 183
Db 692 GAG 694
RESULT 8
US-09-611-659A-3
; Sequence 3, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Mao, Long
; APPLICANT: Rod, Wang
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611,659A
; CURRENT FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; US-09-611-659A-3
Alignment Scores:
Pred. No.: 5.47e-26 Length: 798
Score: 285.00 Matches: 72
Percent Similarity: 53.74% Conservative: 50
Best Local Similarity: 31.72% Mismatches: 73
Query Match: 23.44% Indels: 32
DB: 4 Gaps: 6
US-10-069-527-4 (1-232) x US-09-611-659A-3 (1-798)
Qy 1 MetAlaargGlyLysIleGlnIleLysLeuIleGluAsnGlnThrAspArgGlnValThr 20

```

Db      1  ATGGCTAGAGAAAAATTCAAGATCAAGAAATAGTAATCTCCACAGCAAGCAAGTTCACA 60
Qy      21  Tysrlyrsarqarqanqlyllepheylslysalaglnlueuthrvalleucysasp 40
        61  TTTTCAAGAGAGAGAGAGAGTTTATTCAGAGAAAGTGAGAGAACTTCTGCTCTGAGAT 120
Qy      41  Alalysvalserleuilemetleuseranthrasnlymechisglutyrilleserpro 60
        121  GCTGATGTTGCTCTCATCATTTCTCTTCTACTGAGAAATATTAATGACTATTCAGTCA 180
Qy      61  ThrThrThr-----Thlysermetyrasaptyr 71
        181  AGCATGAAACAAATTCCTGAGAGCGGTGATTTGCTTCCAAAATCTGAGAAAATTTGAT 240
Qy      72  Glnlysrhmetglyleaspleutrpargthrhisgluglusermetlyasprthleu 91
        241  CAACCATCACTGAACTTCAGCTTGTAGAAAATAGCAACTACTCCAGATTAGC----- 294
Qy      92  Trplysleuylsglulleasnslyrleuargarglulleargllyrhis 111
        295  -----AAGGAAATTTCCGAAAAAAGTCATCGA---TTAAGCAATAGAGGAGAA 342
Qy      112  Aspleuansglyleuserpheaspluleualaserleuaspsaspglumetglnser 131
        343  GAACCTTCAAGAGACTAAATTTGAGAGATTGCAACAAATTGAGAGATCTTGAAACTCGA 402
Qy      132  Leuasppalalleargllyr----- 139
        403  TTGAGCCGCGTCATAGAGAGAAAGGTGATTAATATATGAGAGATCAACCACTCCAA 462
Qy      140  -----Tyrlisvallellysrhnglnthrhisgluglusermetlyasprthleu 156
        463  CAAAAGGATGATCACTTAATGAGAA---GAAATGAAAAATTAAGCAACAGTGTAGAG 519
Qy      157  Leugluginargarglyasmetleuhsiglytyrphasplgluallaaglyglu 176
        520  ATATCTAATATATATATATATATATATATATATATATATATATATATATATATATAT 579
Qy      177  Aspproglntrglytyrgluaspsanglucly---Aspyrcluserlaleualaleu 195
        580  GAACCGAGAAATGAGATTATATATATATATATATATATATATATATATATATATATAT 639
Qy      196  Serasnglylalaasnauleu 202
        640  ACAATCCATGTAACTCAATT 660
Db
RESULT 9
US-09-611-659A-2
; Sequence 2, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Mao, Long
; APPLICANT: Rod, Wing
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611,659A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1010
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-611-659A-2

Alignment Scores:
Pred. No.: 7 79%-26
Score: 285.00
Percent Similarity: 53.74%
Best Local Similarity: 31.72%
Query Match: 23.44%
DB: 4
Length: 1010
Matches: 72
Conservative: 50
Mismatches: 53
Indels: 32
Gaps: 6

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US-10-069-527-4 (1-232) x US-09-611-659A-2 (1-1010)
Qy      1  MetAlarqglylylleglulleuileglnsnglnthrashnrglnvalthr 20
        79  ATGGCTAGAGAAAAATTCAAGATCAAGAAATAGTAATCTCCACAGCAAGCAAGTTCACA 138
Db
Qy      21  Tysrlyrsarqarqanqlyllepheylslysalaglnlueuthrvalleucysasp 40
        139  TTTTCAAGAGAGAGAGAGTTTATTCAGAGAAAGTGAGAGAACTTCTGCTCTGAGAT 198
Qy      41  Alalysvalserleuilemetleuseranthrasnlymechisglutyrilleserpro 60
        199  GCTGATGTTGCTCTCATCATTTCTCTTCTACTGAGAAATATTAATGACTATTCAGTCA 258
Qy      61  ThrThrThr-----Thlysermetyrasaptyr 71
        259  AGCATGAAACAAATTCCTGAGAGCGGTGATTTGCTTCCAAAATCTGAGAAAATTTGAT 318
Qy      72  Glnlysrhmetglyleaspleutrpargthrhisgluglusermetlyasprthleu 91
        319  CAACCATCACTGAACTTCAGCTTGTAGAAAATAGCAACTACTCCAGATTAGC----- 372
Qy      92  Trplysleuylsglulleasnslyrleuargarglulleargllyrhis 111
        373  -----AAGGAAATTTCCGAAAAAAGTCATCGA---TTAAGCAATAGAGGAGAA 420
Qy      112  Aspleuansglyleuserpheaspluleualaserleuaspsaspglumetglnser 131
        421  GAACCTTCAAGAGACTAAATTTGAGAGATTGCAACAAATTGAGAGATCTTGAAACTCGA 480
Qy      132  Leuasppalalleargllyr----- 139
        481  TTGAGCCGCGTCATAGAGAGAAAGGTGATTAATATATGAGAGATCAACCACTCCAA 540
Qy      140  -----Tyrlisvallellysrhnglnthrhisgluglusermetlyasprthleu 156
        541  CAAAAGGATGATCACTTAATGAGAA---GAAATGAAAAATTAAGCAACAGTGTAGAG 597
Qy      157  Leugluginargarglyasmetleuhsiglytyrphasplgluallaaglyglu 176
        598  ATATCTAATATATATATATATATATATATATATATATATATATATATATATATATAT 657
Qy      177  Aspproglntrglytyrgluaspsanglucly---Aspyrcluserlaleualaleu 195
        658  GAACCGAGAAATGAGATTATATATATATATATATATATATATATATATATATATATAT 717
Qy      196  Serasnglylalaasnauleu 202
        718  ACAATCCATGTAACTCAATT 738
Db
RESULT 10
US-08-867-087B-12
; Sequence 12, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarkist Sparkman Campbell Leigh &
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible

```



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OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,0878
FILING DATE: June 2, 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/323,449
FILING DATE: October 14, 1994
APPLICATION NUMBER: U.S. 08/485,981
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO. 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1043 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
US-08-867-087B-12

Alignment Scores:
Pred. No.: 2.57e-25 Length: 1043
Score: 281.00 Matches: 75
Percent Similarity: 50.48% Conservative: 83
Best Local Similarity: 36.06% Mismatches: 83
Query Match: 23.11% Indels: 20
DB: Gaps: 6

US-10-069-527-4 (1-232) x US-08-867-087B-12 (1-1043)
QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 34 ATGGGAGGCGAAGAGTTGAGCTGACGACGACGACGACGACGACGACGACGACGACGAC 93
QY 21 TySerIysArgArgAsnGlyIlePheLysLysAlaGlnIleuThrValLeuCyAsp 40
DB 94 TTCGCCAAGCGCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 153
QY 41 AlaIysValSerLeuIleMetLeuSerAsnThrAsnLysMetIleGluIleSerPro 60
DB 154 GCCAGGTCGGCTCATCATCTTCTCCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 213
QY 61 ---ThrThrThrThrLysSerMetTyT-----AspAspTyT 71
DB 214 GGCATACCAAGACTTAGAAGATGACCAATGTTGCTACAAATGCTCAAGTTCACAC 273
QY 72 GlnIysThrMetGlyIleAspLeuThrArgThrHisGlnGlnSerMetLysAspThrLeu 91
DB 274 AATGCATCTTCTGAACTCAGAGCTGG---TACCATGAAATGCA----- 315
QY 92 TrpLysLeuLysGluIleAsnAsnLysLeuArgArgGlnIleArgGlnArgLeuGlyHis 111
DB 316 ---AAGTTGAAGCAAAATTGAAGCTTTCACGCGACCTCAAGGACACTTCTGGGGAG 372
QY 112 AspLeuAsnGlyLeuSerPheAspGlnLeuAlaSerLeuAspAspGlnMetGlnSerSer 131
DB 373 GATCTTGACCACTGACCGTCGAAGAAATGCGACAGCTGAGAAACAGCTTGAAATGCA 432
QY 132 LeuAspAlaIleArgGlnArgLysTyHisValIleLysThrGlnThrHisThrLys 151
DB 433 CTATCAGAGCGGACGACGAGAAAGACGACCACTATATGACAGAGTGAAGGAACTTCC 492
QY 152 LysLysValLysAsnLeuGlnArgArgGlyAsnMetLeuHisGlyTyPheAspGln 171
DB 493 AGAAGAGCGGTGAGCTGGGTGAATTAATAGCAACTCAGAC-----AAGCTC 543
QY 172 GluAlaIleGlyLysAspProGlnIleTyArgIleGluAspAsnGlnGlyAspTyArgLys 191
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DB 544 GAGCTTGAGGTTCCACGACACTAC---AAGACCATGACGACGACCTCTGGGCTGAG 600
QY 192 AlaLeuAlaLeuSerAsnGlyAla 199
DB 601 GCGCGCGGTGATGAGATGCGCC 624

RESULT 11
US-09-067-800-1
Sequence 1, Application US/09067800
Patent No. 6198024
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Seed Plants Characterized by Delayed
TITLE OF INVENTION: Seed Dispersal
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,800
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..827
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1062
OTHER INFORMATION: /notes= "There is a poly(A) tail at
OTHER INFORMATION: the end."
US-09-067-800-1
Alignment Scores:
Pred. No.: 3.51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: Gaps: 7

US-10-069-527-4 (1-232) x US-09-067-800-1 (1-1062)
QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20
```



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; LOCATION: (1061)
; US-09-105-652-1
Alignment Scores:
Pred. No.: 3,51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: 3 Gaps: 7

US-10-069-527-4 (1-232) x US-09-105-652-1 (1-1062)
Oy 1 MetAlaArgGlyLysIleGluIleValSerLeuAlaSerLeuAspGluValThr 20
Db 101 ATGGAGAGAGTAGGTTCACTGAGAGAGATGAGAACCAATCAATGAGCAAGTTACT 160
Oy 21 TySerLysArgAsnGlyIlePheLysValGlnGluLeuThrValLeuCyAsp 40
Db 161 TTCTCAAGAGAGAGTGTGTTGCTCAAGAAAGCTCAATGAGATCTGTTCTTCGCAT 220
Oy 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
Db 221 GCTGAGGTGCTCTCATGCTCTTCTTCCAAAGCAAACTCTGAAATATTCACCGAC 280
Oy 61 ThrThrThrThrLysSerMet-----TyrAspAspTyr-----GlnLysThr 74
Db 281 TCTTGCATGAGAGAGATCTTGAACGCTATGATCGTATTATATTCAGACAAACAATT 340
Oy 75 MetGlyIleAspLeuTyrArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeu 94
Db 341 GTTGCCGAGAGCGTTTCCAAAGTGAAT-----TGGGTTCTA 379
Oy 95 LysGluIleAsnAsnLysLeuArgArgGluIle-----ArgGlnArgLeu 109
Db 380 GAAACATGCTAAGCTCAAGCAAGAGTTGAGTCTTGAGAAACAACAAAGAAATTTATG 439
Oy 110 GlyHisAspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspGluMetGln 129
Db 440 GGGGAAGATCTTGATTCGTTGAGCTTGAGAGCTCCAAAGCTTGAGACATCAGTCAT 499
Oy 130 SerSerLeuAspAlaIleArgGlnArgLysTyrHisValIleLysThrGlnThr 149
Db 500 GCAGCTATCAAGAGATTAGTCAAGAAACCAAGCTATGTTGAAATCCATATCTGCG 559
Oy 150 ThrLysLysValLysAsnLeuGlnArgArgGlyAsnMetLeuHisGlyTyrPhe 169
Db 560 CTCGAGAGAGAGATTAAGCTTGCAAGATCAACAATTCGCTTCAAAAAGATTAG 619
Oy 170 AspGlnGlu---AlaAlaGlyGluAsp-----ArgGlnArgLeu 177
Db 620 GAGAGGAGAGAGAAAGCGGTGACAGAGAGCAATTAGTCAATGCTCAACTCTTCT 679
Oy 178 -----ProGlnTyrGlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeu 193
Db 680 TCAAGTCTTCTGCTCAATATCGGTAACTCTCCAGAGATGCGTTGTGAGAGAGTT 739
Oy 194 AlaLeuSerAsnGlyAlaAsnAsnLeuTyrThrPheHisLeuHisProAsn 211
Db 740 GGGGAGAGAGACGCTGTCATCGTCTGACG-----GAACCAAC 781

RESULT 12
US-09-105-652-1
; Sequence 1, Application US/09105652
; Patent No. 6239068
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Martienssen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/105,652
; EARLIER FILING DATE: 1998-06-26
; EARLIER APPLICATION NUMBER: 60/051,030
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101) ..(826)
; FEATURE:
; NAME/KEY: polyA_signal

```

```

; LOCATION: (1061)
; US-09-105-652-1
Alignment Scores:
Pred. No.: 3,51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: 3 Gaps: 7

US-10-069-527-4 (1-232) x US-09-105-652-1 (1-1062)
Oy 1 MetAlaArgGlyLysIleGluIleValSerLeuAlaSerLeuAspGluValThr 20
Db 101 ATGGAGAGAGTAGGTTCACTGAGAGAGATGAGAACCAATCAATGAGCAAGTTACT 160
Oy 21 TySerLysArgAsnGlyIlePheLysValGlnGluLeuThrValLeuCyAsp 40
Db 161 TTCTCAAGAGAGAGTGTGTTGCTCAAGAAAGCTCAATGAGATCTGTTCTTCGCAT 220
Oy 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
Db 221 GCTGAGGTGCTCTCATGCTCTTCTTCCAAAGCAAACTCTGAAATATTCACCGAC 280
Oy 61 ThrThrThrThrLysSerMet-----TyrAspAspTyr-----GlnLysThr 74
Db 281 TCTTGCATGAGAGAGATCTTGAACGCTATGATCGTATTATATTCAGACAAACAATT 340
Oy 75 MetGlyIleAspLeuTyrArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeu 94
Db 341 GTTGCCGAGAGCGTTTCCAAAGTGAAT-----TGGGTTCTA 379
Oy 95 LysGluIleAsnAsnLysLeuArgArgGluIle-----ArgGlnArgLeu 109
Db 380 GAAACATGCTAAGCTCAAGCAAGAGTTGAGTCTTGAGAAACAACAAAGAAATTTATG 439
Oy 110 GlyHisAspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspGluMetGln 129
Db 440 GGGGAAGATCTTGATTCGTTGAGCTTGAGAGCTCCAAAGCTTGAGACATCAGTCAT 499
Oy 130 SerSerLeuAspAlaIleArgGlnArgLysTyrHisValIleLysThrGlnThr 149
Db 500 GCAGCTATCAAGAGATTAGTCAAGAAACCAAGCTATGTTGAAATCCATATCTGCG 559
Oy 150 ThrLysLysValLysAsnLeuGlnArgArgGlyAsnMetLeuHisGlyTyrPhe 169
Db 560 CTCGAGAGAGAGATTAAGCTTGCAAGATCAACAATTCGCTTCAAAAAGATTAG 619
Oy 170 AspGlnGlu---AlaAlaGlyGluAsp-----ArgGlnArgLeu 177
Db 620 GAGAGGAGAGAGAAAGCGGTGACAGAGAGCAATTAGTCAATGCTCAACTCTTCT 679
Oy 178 -----ProGlnTyrGlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeu 193
Db 680 TCAAGTCTTCTGCTCAATATCGGTAACTCTCCAGAGATGCGTTGTGAGAGAGTT 739
Oy 194 AlaLeuSerAsnGlyAlaAsnAsnLeuTyrThrPheHisLeuHisProAsn 211
Db 740 GGGGAGAGAGACGCTGTCATCGTCTGACG-----GAACCAAC 781

RESULT 13
US-09-349-677-1
; Sequence 1, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP

```

```

/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/349,677
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/067,800
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1062 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 101..827
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1062
/ OTHER INFORMATION: /note= "There is a poly(A) tail at
/ OTHER INFORMATION: /note= "There is a poly(A) tail at
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..1062
/ OTHER INFORMATION: /note= "Nucleotide and Deduced
/ OTHER INFORMATION: Amino Acid Sequences of the AGR8 cDNA clone."
US-09-349-677-1

Alignment Scores:
Pred. No.: 3.51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: 3 Gaps: 7

US-10-069-527-4 (1-232) x US-09-349-677-1 (1-1062)
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QY 21 TySerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
DB 161 TTCTCAAAAGAGAGGTGTGGTTGCTCAAGAAAGCTCAGATCTCTGTTCTTCGCAAT 220
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 221 GCTGAGGTTCTCTCATCGTCTCTCTTCCAAAGCAAACTCTTCGAATATTCACCGAC 280
QY 61 ThrThrThrThrLysSerMet-----TyrAspAspTyr-----GlnLysThr 74
DB 281 TCTTGATGAGAGGATCTTGAACGCTATGATCGCTATTATTAATTCAGACAAACAACTT 340
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DB 341 GTTGGCCGAGAGCTTTCACAAAGTGAAT-----TGGTTCTCA 379
QY 95 LysGluIleAsnAsnLysLeuArgGluIle-----ArgGlnArgLeu 109
DB 380 GAACATGCTTAAGCTCAAGGCAAGAGTTGAGTACTTGAGAACAAACAAAGAAATTTATG 439
QY 110 GlyHisAspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspGluMetGln 129
DB 440 GGGAGATCTTGCATTCCTGAGCTTGAAGAGCTCCAAAGCTTGAGACATCAGCTCGAT 499
QY 130 SerSerLeuAspAlaIleArgGlnArgLysTyrHisValIleLysThrGlnThrGluThr 149
DB 500 GGAGCTATCAAGAGATTGATGTCAGAAACCAAGCTATGTCATTCATCTCG 559
QY 150 ThrLysLysValLysAsnLeuGluGlnArgGlyAsnMetLeuHisGlyTyrPhe 169
DB 560 CTCGAGAGAGAGATTAAGCCCTTGCAGATCAACAATTCGCTTCAAAAAGATTAG 619
QY 170 AspGlnGlu-----AlaAlaGlyGluAsp----- 177
DB 620 GAGAGGAGAGAGAAACGGGTGACAGAGACAAATTATGCTCAACTCTTCT 679
QY 178 -----ProGlnTyrGlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeu 193
DB 680 TCAGTCTTTCGCTCAATTAAGCTGAACCTCTCCAGATGCTTGTGAGAGAGCTT 739
QY 194 AlaLeuSerAsnGlyAlaAsnAsnLeuTyrThrPheHisLeuHisProAsn 211
DB 740 GGGGAGAGAGAACGGTGTGATCGTTCGTTGACG-----GAACCAAC 781

RESULT 14
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/ Sequence 1, Application US/09708584
/ Patent No. 6541683
/ GENERAL INFORMATION:
/ APPLICANT: Yancofsky, Martin F.
/ APPLICANT: Marienssen, Robert
/ APPLICANT: Ferrandiz, Cristina
/ APPLICANT: Gu, Qing
/ TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
/ FILE REFERENCE: P-UD 3040
/ CURRENT APPLICATION NUMBER: US/09/708,584
/ PRIOR FILING DATE: 2000-11-07
/ PRIOR APPLICATION NUMBER: 09/105,652
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/051,030
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1062
/ TYPE: DNA
/ ORGANISM: Arabidopsis sp.
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(826)
/ NAME/KEY: polyA signal
/ LOCATION: (1061)
US-09-708-584-1

Alignment Scores:
Pred. No.: 3.51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: 4 Gaps: 7

US-10-069-527-4 (1-232) x US-09-708-584-1 (1-1062)
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QY 194 AlaIeuSerAsnGlyAla-----AsnIeuLeuTythrPheHisIeuHis 209
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QY 210 ProAsn 211
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Search completed: September 26, 2004, 11:14:11
 Job time : 76.1432 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: September 26, 2004, 07:03:56 ; Search time 473.861 Seconds
(without alignments)
2479.773 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARKERIKLENTNQT.....HGGSSIGSITLHDLRLA 232

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Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	709.5	58.3	946	15	US-10-104-580-2	Sequence 2, Appl1
3	655.5	53.9	1050	13	US-10-428-114-12758	Sequence 12758, A
4	652	53.6	1221	13	US-10-428-114-15025	Sequence 15025, A
5	640.5	52.7	1221	13	US-10-428-114-11957	Sequence 11957, A
6	631.5	51.9	1155	13	US-10-424-559-66649	Sequence 66649, A
7	612	50.3	644	17	US-10-021-323-8631	Sequence 8631, Ap
8	604.5	49.7	1036	13	US-10-424-559-120794	Sequence 120794, A
9	576.5	47.4	871	13	US-10-425-114-10670	Sequence 10670, A
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13	471	38.7	2718	13	US-10-424-559-130795	Sequence 130795, A
14	454	37.3	407	12	US-09-922-293-3294	Sequence 3294, A
15	435	35.8	425	12	US-09-922-293-14	Sequence 14, Appl
16	419.5	34.5	4285	15	US-10-104-580-1	Sequence 1, Appl
17	410	33.7	401	12	US-09-922-293-15	Sequence 15, Appl
18	410	33.7	432	12	US-10-437-965-28598	Sequence 28598, A
19	398	32.7	928	17	US-10-437-965-28598	Sequence 3447, Ap
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33	349	28.7	309	12	US-09-732-627A-337	Sequence 380, App
34	347	28.5	340	12	US-09-732-627A-380	Sequence 3293, Ap
35	332	27.3	298	12	US-09-922-293-3293	Sequence 238, App
36	331.5	27.3	896	15	US-10-278-536-238	Sequence 55, Appl
37	331.5	27.3	896	13	US-10-412-699B-55	Sequence 3293, Ap
38	327	26.9	285	12	US-09-922-293-3292	Sequence 7, Appl
39	326	26.8	10140	15	US-10-094-458A-7	Sequence 3442, Ap
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42	313	25.7	3265	17	US-10-437-963-9922	Sequence 1150, Ap
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ALIGNMENTS

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Sequence 3, Application US/10104580
Publication No. US2003035628A1
GENERAL INFORMATION:
APPLICANT: Strauss et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 62486
CURRENT APPLICATION NUMBER: US/10/104,580
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 09/410,464
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 09/287,700
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: 60/080,851
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 681
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa

FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(681)
US-10-104-580-3

Alignment Scores:

Pred. No.: 3,786-75 Length: 681
Score: 709.50 Matches: 149
Percent Similarity: 72.38% Conservative: 24
Best Local Similarity: 62.34% Mismatches: 45
Query Match: 58.35% Indels: 21
DB: 15 Gaps: 5

US-10-069-527-4 (1-232) x US-10-104-580-3 (1-681)

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DB 181 TCACATGACAGAAAGAAATGATACATCAATATCAGAAAGCTTATGACATAGATCTGTGG 240
QY 81 ArgThrHisGluLysSerMetLysAspThrLeuTrpLysLeuLysGluIleAsnAsnLys 100
DB 241 GGCACTCAATACGAGAAATGCAAGACACACTGAGAACTGATCATCATCAATCAATAG 300
QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGln 120
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QY 181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
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QY 201 AsnLeuTyrThrPheHisLeuHis-----ProAsnLeu 212
DB 580 AACCTCATCATTCCTCCCTGATTCACGGGCAACACCAACCAACCATCTCCCTAATCTT 639
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RESULT 2

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Sequence 2, Application US/10104580
Publication No. US20030033628A1
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 62486
CURRENT APPLICATION NUMBER: US/10/104,580

CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 09/410,464
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 09/287,700
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: 60/080,851
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 946
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(684)
US-10-104-580-2

Alignment Scores:

Pred. No.: 6,136-75 Length: 946
Score: 709.50 Matches: 149
Percent Similarity: 72.38% Conservative: 24
Best Local Similarity: 62.34% Mismatches: 45
Query Match: 58.35% Indels: 21
DB: 15 Gaps: 5

US-10-069-527-4 (1-232) x US-10-104-580-2 (1-946)

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DB 61 TACTGAGAGAGAAAGAAATGATATTTCAGAAAGCCCAAGAACTCACTGACTTGTGAT 120
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DB 181 TCACATGACAGAAAGAAATGATACATCAATATCAGAAAGCTTATGACATAGATCTGTGG 240
QY 81 ArgThrHisGluLysSerMetLysAspThrLeuTrpLysLeuLysGluIleAsnAsnLys 100
DB 241 GGCACTCAATACGAGAAATGCAAGACACACTGAGAACTGATCATCATCAATCAATAG 300
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QY 201 AsnLeuTyrThrPheHisLeuHis-----ProAsnLeu 212
DB 580 AACCTCATCATTCCTCCCTGATTCACGGGCAACACCAACCAACCATCTCCCTAATCTT 639
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Db      640 CACCTT---GGAGATGATTTGGAGCC-----CATGAACCTTGGCCTT 678
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-26
; NUMBER OF SEQ ID NOS: 73126
; SEQ ID NO 12758
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701209467_FLI
US-10-425-114-12758

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Best Local Similarity: 59.17% Mismatches:      51
Query Match:    53.91%       Indels:       15
DB:             13           Gaps:         7

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DB      118 TACTCCAGGCGAAGATGTGATCTTCAAGAAAGCTCAAGAACTGATGCTCTGTGAT 177
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
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QY      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGly---IleAspLeu 79
DB      238 GGCCTCAGCAAAAAGATCATGTGATCATGATCAGAGACTTGGGGATATTGATCTG 297
QY      80 TTPAArgThrHisGluGlnSerMetLysAspThrLeuTTPylsLeuLysGluIleAsn 99
DB      298 TGGCGTTCTCACTATGAGAAATGCTTGAAGCTTGAAGAGCTATGATTTAAACAC 357
QY      100 LysLeuArgArgGluIleArgGlnArgLeuGlyHis-----AspLeuAsnGlyLeuSer 117
DB      358 AAGCTCAGAGACAGATCATGCGATGAGATGAGGCTTGGATGATGACAGCATGAGC 417
QY      118 PheAspGluLeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGln 137
DB      418 TTCACGCAACTCGCAGCTCTTGAAGAGATTGGTTCTTCATAGGGGAAAATACGAA 477
QY      138 ArgLysTyrHisValIleLysThrGlnThrGluThrThrLysLysValLysAsnLeu 157
DB      478 CGAAGTTCCACGTGATCAAAACAGCATGATCACTGACAGAAAAGTTTAAAGCTCG 537
QY      158 GluGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleGlyLeuAsp 177
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DB      646 GGGCGCTTCACCTGATGCGTTCTGTGATCAGACATTCATCTGAAACCTTCCCTCC 705
QY      213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeuAla 232
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; Sequence 15025, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73126
; SEQ ID NO 15025
; LENGTH: 1231
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3043-050-F6_FLI
US-10-425-114-15025

Alignment Scores:
Pred. No.:      7e-68      Length:      1231
Score:          652.00     Matches:      143
Percent Similarity: 70.45% Conservative: 31
Best Local Similarity: 57.89% Mismatches:      53
Query Match:    53.62%     Indels:       20
DB:             13         Gaps:         8

US-10-069-527-4 (1-232) x US-10-425-114-15025 (1-1231)
QY      1 MetAlaArgGlyLysIleGluIleLeuSerLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB      264 ATGGGTGCGAGCAAGATTAAGTAAAGTTGATGGAAGCCCAACAGGCAAGTCACT 323
QY      21 TyrSerLysArgArgAsnGlyIlePheLysAlaGlnGluLeuThrValLeuCysAsp 40
DB      324 TACTCCAGGCGAAGATGTGATCTTCAAGAAAGCTCATGAACTGATGCTCTGTGAT 383
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB      384 GCCAAGGTTTCACTTATCATGTTCTTAAACAAACAGATGATGATTAACCTTACCTT 443
QY      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGly---IleAspLeu 79
DB      444 GGCCTCAGCAAAAAGATCATGTGATCATGATCAGAGACTTGGGGATATTGATCTG 503
QY      80 TTPAArgThrHisGluGlnSerMetLysAspThrLeuTTPylsLeuLysGluIleAsn 99
DB      504 TGGCATTTCTCATATGAGAAATGCTTGAAGACTTGAAGAGCTTGAAGATTTAAACAT 563
QY      100 LysLeuArgArgGluIleArgGlnArgLeuGlyHis-----AspLeuAsnGlyLeuSer 117
DB      564 AAGCTCAGAGACAGATCATGCGATGAGATGAGGCTTGGATGATGACAGCATGAGC 623
QY      118 PheAspGluLeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGln 137

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Db 624 TTCGCGCACTGCCGCACTCTTGAAGAGATATGCTTTCATCCATAGGGAATAATCCGGA 663
QY 138 ArglyrYrHsValIlelyeThrGlnThrThrlYslyValIyAsnLeu 157
Db 684 GAAAGTTTCACGATCAAACTCGACATGATCCGTAGGAAAAGGTTAAAGCCTG 743
QY 158 GluGlnArgArGlyAsnMetLeuHs61YrPheAspGlnGluIleAlaGlyGluAsp 177
Db 744 AAGCAGATGATGGAAATGCTGCTG-----CTTGAACCTGAAAGCTGTGATCCAT 794
QY 178 ProGlnYrGlyYrGluAspAsnGluGlyAspYrGluSer----- 191
Db 795 CCACAATTTCTTTTGGACAGAT---GAAAGAGACAGAGAAATCAGCAGCAGCAGCAGCA 851
QY 192 ---AlaLeuAlaLeuSerAsnGlyAlaAsnAsnLeuYrThrPhe---HisLeuHis 209
Db 852 GCACACAGTGCACCTGGCCACAGGTCCTCCACCTGTATGATCTGTCTATCGACACAT 911
QY 210 ProAsnLeu-----HisHisGlyGlySerSerLeuGlySerSerIleThrHis 225
Db 912 TCTCATCTGAACCTTTTCTCCCACTTCTAATGAGAGAGCAACCTTTAAACTGAT 971
QY 226 LeuHisAspLeuArgLeuAla 232
Db 972 ---CATGACCTTCGCTTGCCT 989

RESULT 5
US-10-425-114-11957
; Sequence 11957, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11957
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701148021_FLI
US-10-425-114-11957

Alignment Scores:
Pred. No.: 1,63e-66 Length: 1212
Score: 640.50 Matches: 142
Percent Similarity: 70.04% Conservative: 31
Best Local Similarity: 57.49% Mismatches: 55
Query Match: 52.67% Indels: 19
DB: 13 Gaps: 8

US-10-069-527-4 (1-232) x US-10-425-114-11957 (1-1212)
QY 1 MetAlaArgGlyYsIleGluIleGlyLeuIleGluAsnGlnThrAsnArgGlnValThr 20
Db 232 ATGGGTGCTGGCAAGATTGATTAAGTTGATTGAGAACCCACCAAGCAGCAAGTACACC 291
QY 21 TySerIleArgArgAsnGlyIlePheIlyValAlaGlnGluLeuThrValLeuCyAsp 40
Db 292 TACTCCAGGAGGAGATGATCTTCAAGAAAGCCTCAGTGTCTCTGTAT 351
QY 41 AlaIyValSerLeuIleMetLeuSerAsnThrAsnIyMetHs61YrYrIleSerPro 60
Db 352 GCCAAGTTTCATCTATCATGTTCTCTAATAACACAAATGCAATGATTAACCTTACCTT 411

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QY 61 ThrThrThrThrIleSerMetYrAspAspYrGlnIlyThrMetGly---IleAspLeu 79
Db 412 GGCCTCCACACAAAAGATATGATCATGATCAAGAAAGACTTTGGGGATATGATCTG 471
QY 80 TPATrThrHsGluGluSerMetYsAspThrIleuTrpYsLeuYsGluIleAsnAsn 99
Db 472 TGGCATCTGCATAGAGAAAATGCTTGAATAACTGGAAGAGCTGAAGATATTACAT 531
QY 100 YsLeuAlaGlyGluIleArgGlnArgLeuGlyHis-----AspLeuAsnGlyLeuSer 117
Db 532 AAGCTCGGAGACACATAGCATAGATGATGAGGCTTGGACATGACAGACATGAGC 591
QY 118 PheAspGlnLeuAlaSerIleuAspAspGluMetGlnSerSerIleuAspAlaIleArgGln 137
Db 592 TTCGCGCACTGCCGCACTCTTGAAGAGATATGCTTTCATCCATAGGGAATAATCCGGA 651
QY 138 ArglyrYrHsValIlelyeThrGlnThrThrlYslyValIyAsnLeu 157
Db 652 GAAAGTTTCACGATCAAACTCGACATGATCCGTAGGAAAAGGTTAAAGCCTG 711
QY 158 GluGlnArgArGlyAsnMetLeuHs61YrPheAspGlnGluIleAlaGlyGluAsp 177
Db 712 AAGCAGATGATGGAAATGCTGCTGCTTGAACCTT-----AAGGAAAAGCTGTGATCCAT 765
QY 178 ProGlnYrGlyYrGluAspAsnGluGlyAspYrGluSer----- 191
Db 766 CCACAATTTCTTTTGGACAGAT---GAAAGAGACAGAGAAATCAGCAGCAGCAGCAGCA 822
QY 192 ---AlaLeuAlaLeuSerAsnGlyAlaAsnAsnLeuYrThrPhe---HisLeuHis 209
Db 823 GCACACAGTGCACCTGGCCACAGGTCCTCCACCTGTATGATCTGTCTATCGACACAT 882
QY 210 ProAsnLeu-----HisHisGlyGlySerSerLeuGlySerSerIleThrHis 225
Db 883 TCTCATCTGAACCTTTTCTCCCACTTCTAATGAGAGAGCAACCTTTAAACTGAT 942
QY 226 LeuHisAspLeuArgLeuAla 232
Db 943 ---CATGACCTTCGCTTGCCT 960

RESULT 6
US-10-424-599-66649
; Sequence 66649, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 66649
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31198C.1
US-10-424-599-66649

Alignment Scores:
Pred. No.: 1,82e-65 Length: 1155
Score: 631.50 Matches: 141
Percent Similarity: 70.04% Conservative: 32
Best Local Similarity: 57.09% Mismatches: 55
Query Match: 51.93% Indels: 19
DB: 13 Gaps: 8

US-10-069-527-4 (1-232) x US-10-424-599-66649 (1-1155)

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QY      1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAspArgGlnValThr 20
DB      111 ATGGGCTCGAGGCAAGATGAGTAAAGTTGATGGAAGCCACCAAGGCAAGTCACT 170
QY      21 TySerLysArgArgAsnGlyIlePheLeuLysValGlnGluLeuThrValLeuCysAsp 40
DB      171 TACTCCAGCGAAGAGAAAGTATCTTCAGAAAGCTCTGAACTCAAGTCTTCTGAT 230
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB      221 GCCAAGGTTTCATCATGTTCTCTMAAAACAACAGATGATGATTAATGACCT 290
QY      61 ThrThrThrThrThrLysSerMetCysTrpAspArgTyrGlnLysThrMetGly---IleAspLeu 79
DB      291 GGCTTCAGACAAAGAAAGATCATTTGATCATGATCGAAAGACCTTGGGGGATATTTGATCTG 350
QY      80 TrpArgThrHisGluGlnSerMetLysAspThrLeuTyrLysLeuLysGluIleAspAsn 99
DB      351 TGGGCTTCTCACTATGAGAAATGCTTGAATACTGAAGAAAGCTGATGATTAATCAAC 410
QY      100 LysLeuAlaGlyGlnIleArgGlnArgLeuGlyHis-----AspLeuAsnGlyLeuSer 117
DB      411 AAGCTCAAGAAACAGATCAGGCTAGGATAGGTAGGGGTTGGACATGAGACATGAGC 470
QY      118 PheAspGluLeuAlaSerLeuAspArgLumetGlnSerSerLeuAspAlaIleArgGln 137
DB      471 TTCGACCACTCGCAGCTTTCAGAGAGATTTGTTCTTCATAGGAAATACAGAGA 530
QY      138 ArgLysTyrHisValIleLysThrGlnThrGlnThrLysLysValLysAsnLeu 157
DB      531 CGAAAGTTCCAGCTGATCAAAACAGGACTGATCCTCAGGAAAGATTAAGTAAAGCTG 590
QY      158 GluGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyGluAsp 177
DB      591 GAGCGATGAAATAGAGATCTGCTGTTGAACCT---AAGGAAAGTGTGTGATTCAT 644
QY      178 ProGlnTyrGlyTyrGluAspAsnGluGlyAspTyrGlnSer----- 191
DB      645 CCACAAATTTCTTTGACAGAT---GAGGAGACGAGATCAGACGACGACGACAGCA 701
QY      192 ---AlaLeuAlaLeuSerAsnGlyAlaAsnAsnLeuTyrThrPhe---HisLeuHisHis 209
DB      702 GCAGAGAGTTCAGCTGGCCAAACGTCCTCCACCCGTATGCAATCTGTCAACAGACAT 761
QY      210 ProAsnLeu-----HisHisGlyGlySerSerLeuGlySerSerIleThrHis 225
DB      762 TCTCATCTGAACCTTTCTCCACCACTTCTAATGAGAGAACCAACCTTTAAACATGAT 821
QY      226 LeuHisAspLeuArgLeuAla 232
DB      822 ---CATGACCTTCGCCCTTGTCT 839

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RESULT 7
US-10-021-323-8631
; Sequence 8631, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, J111
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Pincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8631
; LENGTH: 644
; TYPE: DNA

```

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; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(644)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3828-013-Q1-K6-F12
US-10-021-323-8631

Alignment Scores:
Pred. No.: 1,67e-63 Length: 644
Score: 612.00 Matches: 118
Percent Similarity: 75.00% Conservative: 38
Best Local Similarity: 56.73% Mismatches: 47
Query Match: 50.33% Indels: 5
DB: 17 Gaps: 2

US-10-069-527-4 (1-232) x US-10-021-323-8631 (1-644)
QY      1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAspArgGlnValThr 20
DB      32 ATGGCTCGAGGCAAGATCCAGATCAAGCTGATGAGAACTCGACCAAGGCAAGTCAAG 91
QY      21 TySerLysArgArgAsnGlyIlePheLeuLysValGlnGluLeuThrValLeuCysAsp 40
DB      92 TATTGGAAGAGAAAGAAACGGTCTTTCAAGAAAGCTAATGAACTTACAGTTCTTTCGAT 151
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB      152 GCTAGAGTTTCATCATGTTTCCATCTGCTGTAACCTCATGATGATTAATCAACCT 211
QY      61 ThrThrThrThrThrLysSerMetCysTrpAspArgTyrGlnLysThrMetGlyIleAspLeu 80
DB      212 TCCACCAACAAGCAAGCAAGATGATGATGATCAGTACCAAGAAACCTTGGGGATTCGATCTG 271
QY      81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB      272 AACCCCATATAGAAAGAAAGCAAGACGCTTACAGAGCTGAAAGGTTAACAGAGAC 331
QY      101 LeuArgArgGlnIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB      332 CTGGCAAAAGATTTAGAGAAAGATGGGCACTGTTGAATGATTTGAGCATCGAAGAT 391
QY      121 LeuHisSerLeuAspArgGluLysGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB      392 CTGGTGCCTTTGGAACAAGAAATGAGAGAGCTGTGCACTTTTGTGATAGAAAGTAT 451
QY      141 HisValIleLysThrGlnThrGlnThrLysLysValLysAsnLeuGlnGlnArg 160
DB      452 CGTCTCTCCCAACGATGATCTTCACGAAAGAGTGAAGATGAGAGATA 511
QY      161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyLysAspProGlnTyr 180
DB      512 CACAAATCTCTTACAT-----GAACCTGAATCCCTGAAAGATGCA---TAT 559
QY      181 GlyTyrGlu---AspAsnGluGlyAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyAla 200
DB      560 GGAATTAAGTTGATTAAGAGGGGATTAATGATACCTGATCGGGTATCAAAATGAGAGTCC 619
QY      200 AsnLeuTyrThrPheHisLeu 207
DB      620 TCGATATTTGCTTACGCTG 641

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RESULT 8
US-10-424-599-120794
; Sequence 120794, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120794
; LENGTH: 1036
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1
US-10-424-599-120794

```

Alignment Scores:

```

Pred. No.: 2,66e-62 Length: 1036
Score: 604.50 Matches: 117
Percent Similarity: 69.47% Conservative: 40
Best Local Similarity: 51.77% Mismatches: 62
Query Match: 49.71% Indels: 7
DB: 13 Gaps: 3

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US-10-069-527-4 (1-232) x US-10-424-599-120794 (1-1036)

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QY 1 MetAlaArgGlyLeuIleGluLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 27 ATGCTCGAGGAAAGATCCAGATCAAGAGATAGAGAACACCAACCCAGCTCACT 86
QY 21 TySerIysArgArgGlnGlyIlePheLeuLeuAlaGlnGluLeuThrValLeuCysAsp 40
DB 87 TATCTAAACGACCGAATGGCTTTTCAGAGGCCCAACAGCTCAACCTTATGCGAT 146
QY 41 AlaIysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluIleAsnLys 60
DB 147 GCCAAGTTTCTATATATATGTTCTCAAGCATGGGAACTCCAGACGATCAAGCC 206
QY 61 ThrThrThrThrLysSerMetTyAspAspTyGlnLysThrMetGlyIleAspLeuTrp 80
DB 207 TCCACCTCAACCAAGGAGCTTCTCGATCAGTACACAGTGAAGTCTAGAGAGCTCTG 266
QY 81 ArgHisIleGluGlnSerMetLysAspThrLeuTrpLysLeuIleAsnLys 100
DB 267 AACTCTATTAACGAAATATGCAAGAACTTGAAGAACTGAAGATGATAGCAAT 326
QY 101 LeuArgArgGluIleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 327 CTTCGTAAAGGAGATTAAGCAGAGAGATGGAGATTTGCTGAACATCTGGGCATGAAAGT 386
QY 121 LeuAlaSerLeuAspArgGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTy 140
DB 387 CTCAGCTCCTTGAGGAAAGATGACACAGCCGCAAGGTTGTTGCTGAGCTAGAT 446
QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160
DB 447 AAGGTGATTAACAATCAGATGACACCCAGAGAAAAGTTTAATACAGAAAGAAAGT 506
QY 161 ArgGlyAsnMetLeuHisGlyTyPheAspGlnGlnAlaIleGlyIleAspProGlnTy 180
DB 507 CACAAACAGCTCCGCGAT-----GACTTGATGCAAAACAAAGATCCACCTTT 557
QY 181 GlyTyGlnLysAsnGlnGlyAspTyGlnSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
DB 558 GCATTGATTAATAGAGAGAGAGATGAGCTGTGATCGGATTCCTCAAAATTAAGTCCA 617
QY 201 AsnLeuTyThrPheHisLeuHis-----HisProAsnLeuHisHisGlyIleSer 218
DB 618 CGCATGTTCGATTAAGACCTTAAGCCAAAGCATCTTAAGTCCCAAGCGAGAGACA--- 674
QY 219 LeuGlySerSerIleThr 224
DB 675 ---GGCTGATCTTACC 689

```

RESULT 9
US-10-425-114-10670
Sequence 10670, Application US/10425114

```

; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yinhua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53233)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10670
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700958586_FLI
US-10-425-114-10670

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Alignment Scores:

```

Pred. No.: 4.67e-59 Length: 871
Score: 576.50 Matches: 112
Percent Similarity: 68.47% Conservative: 40
Best Local Similarity: 50.45% Mismatches: 63
Query Match: 47.41% Indels: 7
DB: 13 Gaps: 3

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US-10-069-527-4 (1-232) x US-10-425-114-10670 (1-871)

```

QY 5 LysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThrTySerLysArg 24
DB 3 AAGATCCAGATCAAGAGATAGAGAACACCAACCCAGGTCATTTCTTCAACGA 62
QY 25 ArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAspAlaLysValSer 44
DB 63 CGGATGCTCTTTCAGAGAGGCCCAAGAGCTCAACCTTCTATGCGATGCCAAGTTCT 122
QY 45 LeuIleMetLeuSerAsnThrAsnLysMetHisGluIleAsnLysSerProThrThrThr 64
DB 123 ATTATTAATGTTCTCAGACATGGGAAACTCCAGAGTAACTCAAGCCCTCACTCAACA 182
QY 65 LysSerMetTyAspAspTyGlnLysThrMetGlyIleAspLeuTrpArgThrHisGlu 84
DB 183 AAGCAGTTCTTCGATCAGTACAGATGAGTCTTAGAGTCTGATCTGAACTGCATTAC 242
QY 85 GluSerMetLysAspThrLeuTrpLysLeuIleAsnLysLeuArgArgGlu 104
DB 243 GAGATATGCAAGAACTTAAGAACTCAAAAGATGTAATAGAAATCTTCGTAAGAG 302
QY 105 IleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeu 124
DB 303 ATTAGGCGAGAGATGGAGATTTGCTGAACGATTTGGGCAATGGAATCTCAAGCTCT 362
QY 125 AspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyHisValIleLys 144
DB 363 GAGAGAGAAAGCAGACAGAGCCGCAAGGTTGTTGCTGAACGTAAAGTAAAGTGAACA 422
QY 145 ThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArgArgGlyAsnMet 164
DB 423 AATGAGATTGACCCCAAGGAAAGTTTAATTAACAGAAAGAGAGCAACAGAGCTC 482
QY 165 LeuHisGlyTyPheAspGlnGlnAlaIleGlyIleAspProGlnTyGlnLysAsp 184
DB 483 CTGCGT-----GACTTGATGCAAGAGCAAGATCCAGCTTTTGCAATGATGAT 533
QY 185 AsnGluLysAspTyGlnSerAlaLeuAlaLeuSerAsnGlyAlaAsnAsnLeuTyThr 204
DB 534 AATGAGAGGAGTACGAGTCTGTGATGCGATTCCTCAAAATTAAGTCCACAGCATGTGCA 593
QY 205 PheHisLeuHis-----HisProAsnLeuHisHisGlyIleSerSerLeuGlySerSer 222

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Db 594 TTGAGCCCTACAGCAAGCCATCTAGTGCACCAAGCGGAGCAGCA-----GGCTTGAT 647
 Oy 223 l1eThr 224
 Db 648 CTNAC 653

RESULT 10
 US-10-260-238-5530
 ; Sequence 5530, Application US/10260238
 ; Publication No. US20040016025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Br1998, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Rieke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 5530
 ; LENGTH: 681
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; US-10-260-238-5530

Alignment Scores:
 Pred. No.: 1,85e-56 Length: 681
 Score: 553.50 Matches: 122
 Percent Similarity: 64.85% Conservative: 33
 Best Local Similarity: 51.05% Mismatches: 63
 Query Match: 45.52% Indels: 21
 DB: 16 Gaps: 7

US-10-069-527-4 (1-232) x US-10-260-238-5530 (1-681)

Oy 1 MetAlaArgGlyLeuIleGluIleLeuLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 1 ATGGGGCGCGGGAAGATCGAATCAAGCGGATCGAAGACCGCAACCGCAAGCGTGAAC 60
 Oy 21 TyrSerLeuArgArgAsnGlyIlePheLeuValAlaGlnIleuThrValLeuCyAsp 40
 Db 61 TACTCCAAAGCGCGGATCGATGAAGAAAGCGCGGACCTGCGTCTGCAC 120
 Oy 41 AlaLeuValSerLeuIleMetLeuSerAsnThrAsnLysMetH1eGluTyrIleSerPro 60
 Db 121 GCCCAGGTGCGCATCTCATCTTCTCTCCACCGGCAAGTACAGAGTCTGCAGCCCC 180
 Oy 61 ThrThrThrThyLysSerMetTyrAspArgTyrGlnLysThrMetGlyIleAspLeuTyr 80
 Db 181 GGAACCGCATGAAGACCACTTTGACCGGTACACAGCGCCATCGGACCGCTATGG 240
 Oy 81 ArgThrH1eGluIleuSerMetLysAspThrLeuTyrLysLeuGluIleAsnLys 100
 Db 241 ATGAGCAGATATGAAATATGACGCCACGCTGAGCATCTCAAGACATCAATCGTGT 300
 Oy 101 LeuArgArgGluIleArgGlnArgLeuGlnH1eAspLeuAsnGlyLeuSerPheArgGlu 120
 Db 301 CTCGCGACAGAGATTAGGCAAGATGGCGGAGATCTGACAGATCTGACACTTGCACGAG 360

Oy 121 LeuAlaSerLeuAspArgGlnMetGlnSerSerLeuAspAlaIleArgGlnArgIleTyr 140
 Db 361 CTCGGCGGCTCGCAAAACGTCAGCGGCTCTTCAAGAGATTCGCATGGAAGTAC 420
 Oy 141 HisValIleLeuThrGlnThrGlnThrThyLysLysValLysAsnLeuGlnArg 160
 Db 421 CATGTATCAGACCGAGACTGATACCTTCAAGAAAAGTGAAGATCGACGAGCGG 480
 Oy 161 ArgGlyAsnMetLeuH1eGlyTyrPheAspGlnAlaAlaGly-----GluSerPro 178
 Db 481 TACAGAACCTG-----CAGCAGAGCTTAGCATGCGGAGAGACCCG 522
 Oy 179 GlnTyrGlyTyrGluAspAsnGly-----AspTyrGluSerAlaLeuAlaLeu 195
 Db 523 GCCTTGGTACGTGACAAACAGCGCGCGCGCTGCGTGGAGACGCGCGCGCGCG 582
 Oy 196 SerAsnGlyAla---AsnAsnLeuTyrThrPheH1eLeu-----HisIleProAsnLeu 212
 Db 583 CTGGCGCGCGCGCGCGCGCATGTACGCTTCCGCGGTGCGCCAGCCAGCCCAACTG 642
 Oy 213 HisH1eGlyCylSerSerLeuGlySerSerIleThrHisLeuH1eAspLeuArgLeu 231
 Db 643 CAC-----GGCATGCGCTTACGCGC-----TTCCACGACCTTCGCGCTG 678

RESULT 11
 US-09-732-627A-4479
 ; Sequence 4479, Application US/09732627A
 ; Publication No. US2004012338A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fincher, Karen L.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21 (51.770) B
 ; CURRENT APPLICATION NUMBER: US/09/732,627A
 ; CURRENT FILING DATE: 2000-12-08
 ; NUMBER OF SEQ ID NOS: 4930
 ; SEQ ID NO 4479
 ; LENGTH: 498
 ; TYPE: DNA
 ; ORGANISM: Gossypium hirsutum
 ; FEATURES:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(498)
 ; OTHER INFORMATION: unsure at all n locations
 ; OTHER INFORMATION: Clone ID: LIB3493-034-Pl-M1-H12
 ; US-09-732-627A-4479

Alignment Scores:
 Pred. No.: 3.34e-54 Length: 498
 Score: 533.00 Matches: 99
 Percent Similarity: 81.29% Conservative: 27
 Best Local Similarity: 63.87% Mismatches: 29
 Query Match: 43.83% Indels: 0
 DB: 12 Gaps: 0

US-10-069-527-4 (1-232) x US-09-732-627A-4479 (1-498)

Oy 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 25 ATGGCTGAGGGAAGATCGACATCAAGCTGATAGAGAACTCGACCAAGGCAAGTCACG 84
 Oy 21 TyrSerLysArgArgAsnGlyIlePheLysValAlaGlnIleuThrValLeuCyAsp 40
 Db 85 TATTCGAAGAGAAAGAGCGGCTTTTCAAGAAAGCTAATGACTTACAGTCTTTGGAT 144
 Oy 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetH1eGluTyrIleSerPro 60
 Db 145 GCTAGGTTTGCATCATCATGTTTTCACACTAGGTAACTCCATGAGTTATTCAGCCCT 204
 Oy 61 ThrThrThrThyLysSerMetTyrAspArgTyrGlnLysThrMetGlyIleAspLeuTyr 80
 Db 205 TCCACCAACAAAGCAAGATATGATGACGAGAAACCTTGGGGAATCATATCTGG 264

```
QY 81 ArgThrHisGluGluSerMetLeuSerPheThrLeuTrpLeuValLeuAsnLys 100
DB 265 AACACCCGCTATGAGAAAATGACAGACGATTGAACGACGCGAAGGCTTAACAGAAC 324
QY 101 LeuAlaSerGluLeuLeuArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 325 CTGCGCAAGAGATTGAGAGAGATGGGCACTGTTGTAATGATTGAGATCGAAGAT 384
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaLeuArgGlnArgLysTyr 140
DB 385 CTGTGCTGTTTGGAACAGAAAATGAGAGCTCTGTCACTTATTCGTGATGAAAATAT 444
QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLys 155
DB 445 CGTGTCTCTCCAAACCAAGATGATATCTTCAGAAAAGAGAG 489

RESULT 12
US-10-425-114-13190
; Sequence 13190, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13190
; LENGTH: 2237
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gm10220148g09_FU1
US-10-425-114-13190

Alignment Scores:
Pred. No.: 3,57e-46 Length: 2237
Score: 474.00 Matches: 87
Percent Similarity: 80.58% Conservative: 25
Best Local Similarity: 62.59% Mismatches: 27
Query Match: 38.98% Indels: 0
Gaps: 0

US-10-069-527-4 (1-232) x US-10-425-114-13190 (1-2237)
QY 1 MetAlaArgGlyLysIleGlnIleLysLeuIleGlnAsnGlnThrAsnArgGlnValThr 20
DB 109 ATGGCTGAGAGAAAGATCCAGATCAAGAGATGAGAAACAAACCCGACGAGTCACT 168
QY 21 TyrSerLysArgArgAsnGlyIlePheLysValGlnGlnLeuThrValLeuCysAsp 40
DB 169 TACTCTAAACGACGAGATGCGCTTTCAAGAACGCCAAGAGCTTACGTTCTCGCAT 228
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnLysIleAspLeuTrp 60
DB 229 GCCAAGGTTTCTATTATGTTCTTCAGACACTGGAACCTCCACCAAGTACATCAGCCCC 288
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
DB 289 TCACCTCAACCAAGAGCTTTCGATCAATACCAATAGATCTGGAGATTATCTCTGG 348
QY 81 ArgThrHisGlnGlnSerMetLysAspThrLeuTrpLysLeuLysGlnIleAsnLys 100
DB 349 AACTCTCATTAACAGAAATGACAGAACTTGAAGAACTGAAGAGGTTGATGAAAT 408
QY 101 LeuArgArgGlnIleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGlu 120
```

```
DB 409 CTTCGTAAGAGATTAGGAGAAATGGAGATTGTCGTAACGACTGGCGCATGGAAGAT 468
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaLeuArgGlnArgLys 139
DB 469 CTCACCTCTTGAAGAAAGAAATGACAAAGCCCGCAAGTTGTTCTGAGCGTAAAG 525

RESULT 13
US-10-424-599-120795
; Sequence 120795, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120795
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1
US-10-424-599-120795

Alignment Scores:
Pred. No.: 1,09e-45 Length: 2718
Score: 471.00 Matches: 86
Percent Similarity: 80.58% Conservative: 26
Best Local Similarity: 61.87% Mismatches: 27
Query Match: 38.73% Indels: 0
Gaps: 0

US-10-069-527-4 (1-232) x US-10-424-599-120795 (1-2718)
QY 1 MetAlaArgGlyLysIleGlnIleLysLeuIleGlnAsnGlnThrAsnArgGlnValThr 20
DB 126 ATGGCTGAGAGAAAGATCCAGATCAAGAGATGAGAAACAAACCCGACGAGTCACT 185
QY 21 TyrSerLysArgArgAsnGlyIlePheLysValGlnGlnLeuThrValLeuCysAsp 40
DB 186 TATCTAAACGACGAGATGCGCTTTCAAGAAAGGCCAAGAGCTCACCGTTCTATGCGAT 245
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnLysIleAspLeuTrp 60
DB 246 GCCAAGGTTTCTATTATGTTCTTCAGACACTGGAAACTCCACAGATGATCAGCCCC 305
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
DB 306 TCACCTCAACCAAGAGCTTTCGATCAATACCAATAGATCTGGAGATTATCTCTGG 365
QY 81 ArgThrHisGlnGlnSerMetLysAspThrLeuTrpLysLeuLysGlnIleAsnLys 100
DB 366 AACTCTCATTAACGAAATGACAGAACTTGAAGAACTGAAGAGTGAATGAAAT 425
QY 101 LeuArgArgGlnIleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 426 CTTCGTAAGAGATTAGGAGAGATGGAGATGTCGTAACGATCTGGGATGAGAAAT 485
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaLeuArgGlnArgLys 139
DB 486 CTCACGCTCTTGAAGAAAGAAATGACAAAGCCCGCAAGTTGTTCTGAGCGTAAAG 542

RESULT 14
US-09-922-293-3294
; Sequence 3294, Application US/09922293
; Publication No. US20040123339A1
; GENERAL INFORMATION:
```

APPLICANT: Conner, Timothy W.
 APPLICANT: Heck, Gregory R.
 APPLICANT: Liu, Jingsong
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 16517.254
 CURRENT APPLICATION NUMBER: US/09/922,293
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: US 60/067,000
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: US 60/069,472
 PRIOR FILING DATE: 1997-12-09
 PRIOR APPLICATION NUMBER: US 60/071,479
 PRIOR FILING DATE: 1998-01-13
 PRIOR APPLICATION NUMBER: US 60/074,201
 PRIOR FILING DATE: 1998-02-10
 PRIOR APPLICATION NUMBER: US 60/074,282
 PRIOR FILING DATE: 1998-02-10
 PRIOR APPLICATION NUMBER: US 60/074,280
 PRIOR FILING DATE: 1998-02-10
 PRIOR APPLICATION NUMBER: US 60/074,281
 PRIOR FILING DATE: 1998-02-10
 PRIOR APPLICATION NUMBER: US 60/074,566
 PRIOR FILING DATE: 1998-02-12
 PRIOR APPLICATION NUMBER: US 60/074,567
 PRIOR FILING DATE: 1998-02-12
 PRIOR APPLICATION NUMBER: US 60/074,565
 PRIOR FILING DATE: 1998-02-12
 PRIOR APPLICATION NUMBER: US 60/075,462
 PRIOR FILING DATE: 1998-02-19
 PRIOR APPLICATION NUMBER: US 60/074,789
 PRIOR FILING DATE: 1998-02-19
 PRIOR APPLICATION NUMBER: US 60/075,459
 PRIOR FILING DATE: 1998-02-19
 PRIOR APPLICATION NUMBER: US 60/075,461
 PRIOR FILING DATE: 1998-02-19
 PRIOR APPLICATION NUMBER: US 60/075,464
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 PRIOR APPLICATION NUMBER: US 60/077,231
 PRIOR FILING DATE: 1998-03-09
 PRIOR APPLICATION NUMBER: US 60/077,229
 PRIOR FILING DATE: 1998-03-09
 PRIOR APPLICATION NUMBER: US 60/077,230
 PRIOR FILING DATE: 1998-03-09
 PRIOR APPLICATION NUMBER: US 60/078,368
 PRIOR FILING DATE: 1998-03-18
 PRIOR APPLICATION NUMBER: US 60/080,844
 PRIOR FILING DATE: 1998-04-07
 PRIOR APPLICATION NUMBER: US 60/083,067
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: US 60/083,386
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: US 60/083,387
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: US 60/083,388
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: US 60/083,389
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: US 60/085,224
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: US 60/085,223
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: US 60/085,222
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: US 60/085,533
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: US 60/086,186
 PRIOR FILING DATE: 1998-05-21
 PRIOR APPLICATION NUMBER: US 60/086,187

PRIOR FILING DATE: 1998-05-21
 PRIOR APPLICATION NUMBER: US 60/086,185
 PRIOR FILING DATE: 1998-05-21
 PRIOR APPLICATION NUMBER: US 60/086,184
 PRIOR FILING DATE: 1998-05-21
 PRIOR APPLICATION NUMBER: US 60/086,183
 PRIOR FILING DATE: 1998-05-21
 PRIOR APPLICATION NUMBER: US 60/086,188
 PRIOR FILING DATE: 1998-05-21
 PRIOR APPLICATION NUMBER: US 60/089,524
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: US 60/089,810
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,814
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,808
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,812
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,807
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,806
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,813
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,811
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/089,793
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: US 60/091,405
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/091,247
 PRIOR FILING DATE: 1998-06-30
 PRIOR APPLICATION NUMBER: US 60/099,667
 PRIOR FILING DATE: 1998-09-09
 PRIOR APPLICATION NUMBER: US 60/099,668
 PRIOR FILING DATE: 1998-09-09
 PRIOR APPLICATION NUMBER: US 60/099,670
 PRIOR FILING DATE: 1998-09-09
 PRIOR APPLICATION NUMBER: US 60/099,697
 PRIOR FILING DATE: 1998-09-09
 PRIOR APPLICATION NUMBER: US 60/100,674
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: US 60/100,673
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: US 60/100,672
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: US 60/100,963
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: US 60/101,131
 PRIOR FILING DATE: 1998-09-21
 PRIOR APPLICATION NUMBER: US 60/101,132
 PRIOR FILING DATE: 1998-09-21
 PRIOR APPLICATION NUMBER: US 60/101,130
 PRIOR FILING DATE: 1998-09-21
 PRIOR APPLICATION NUMBER: US 60/101,508
 PRIOR FILING DATE: 1998-09-22
 PRIOR APPLICATION NUMBER: US 60/101,344
 PRIOR FILING DATE: 1998-09-22
 PRIOR APPLICATION NUMBER: US 60/101,347
 PRIOR FILING DATE: 1998-09-22
 PRIOR APPLICATION NUMBER: US 60/101,343
 PRIOR FILING DATE: 1998-09-22
 PRIOR APPLICATION NUMBER: US 60/101,707
 PRIOR FILING DATE: 1998-09-25
 PRIOR APPLICATION NUMBER: US 60/104,126
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: US 60/104,128
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: US 60/104,127
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: US 60/104,124
 PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: US 60/109,018
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: US 60/108,996
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: US 09/199,129
PRIOR FILING DATE: 1998-11-24
PRIOR APPLICATION NUMBER: US 09/210,297
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 60/111,981
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/113,224
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/229,413
PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 3853
SEQ ID NO 3284
LENGTH: 407
TYPE: DNA
ORGANISM: Glycine max
US-09-922-293-3294

Alignment Scores:
Pred. No.: 7,236-45 Length: 407
Score: 454.00 Matches: 84
Percent Similarity: 83.46% Conservative: 22
Best Local Similarity: 66.14% Mismatches: 21
Query Match: 37.34% Indels: 0
DB: 12 Gaps: 0

US-10-069-527-4 (1-232) x US-09-922-293-3294 (1-407)

QY 1 MetAlaGlyIyIleGluIleGluAsnGlnThrAsnArgGlnValThr 20
DB 25 ATGGCTGAGGAAAGATCCAGATCAAGAGATAGAGAACCCACCGCGGCTCAT 84
QY 21 TyrSerIyArgArgGlnGlyIlePheIyIleAlaGlnGluIleThrValIeuCysAsp 40
DB 85 TATCTTAAAGACGAGATGGCTTTTCAGAGAGCCACGAGCTCCCTTCATGCGAT 144
QY 41 AlaIyValSerIleuIleMetIleSerIleAsnIyMetIyIleSerIlePerp 60
DB 145 GCCAAGTTTCTATTTATTTATGTTCTCCAGCATCGGAACTCCACAGATCATCAGCCCC 204
QY 61 ThrThrThrThrIySerMetIyAspAspIyTyrGlnIyThrMetGlyIleAspIeuTyr 80
DB 205 TCCACCCCAACAAAGAGATCTTCGATCAGTACAGATGATCATCTAGAGATCATCTCG 264
QY 81 ArgThrIsgIuIleuSerMetIyAspThrIleuTyrIyIleuIleAsnIy 100
DB 265 AACTCTCATACGAGATATGCAAGAACTTGAAGAACTGAGATGTGATAGCAT 324
QY 101 LeuArgArgGluIleArgGlnArgIleuGlyIleAspIleuAsnGlyIleuSerPheAspGln 120
DB 325 CTTCGTAAGAGAGATGAGCGAGAGATGAGATGTCGTAACATCTGAGCATGGAAGAT 384
QY 121 LeuAlaSerIeuAspAspGln 127
DB 385 CTCAAGCTCTTGAAGAGAGA 405

RESULT 15
US-09-922-293-14
Sequence 14, Application US/09922293
Publication No. US20040123339A1
GENERAL INFORMATION:
APPLICANT: Comer, Timothy W.
APPLICANT: Heck, Gregory R.
APPLICANT: Liu, Jingdong
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 16517,254
CURRENT APPLICATION NUMBER: US/09/922,293
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/067,000

PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: US 60/069,472
PRIOR FILING DATE: 1997-12-09
PRIOR APPLICATION NUMBER: US 60/071,479
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: US 60/074,201
PRIOR FILING DATE: 1998-02-10
PRIOR APPLICATION NUMBER: US 60/074,282
PRIOR FILING DATE: 1998-02-10
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PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 60/074,565
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 60/075,462
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 60/074,789
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PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: US 60/086,184
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: US 60/086,183
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: US 60/086,188
PRIOR FILING DATE: 1998-05-21

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/ PRIOR FILING DATE: 1998-12-11
/ PRIOR APPLICATION NUMBER: US 60/113,224
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: US 09/229,413
/ PRIOR FILING DATE: 1999-01-12
/ NUMBER OF SEQ ID NOS: 3853
/ SEQ ID NO 14
/ LENGTH: 425
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-922-293-14

Alignment Scores:
Pred. No.: 1,466-42 Length: 425
Score: 435.00 Matches: 84
Percent Similarity: 76.26 Conservative: 22
Best Local Similarity: 60.43 Mismatches: 33
Query Match: 35.77% Indels: 0
Dbs: 12 Gaps: 0

US-10-069-527-4 (1-232) x US-09-922-293-14 (1-425)

Cy 2 AAlargGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThrTyr 21
Db 2 GCGAGAGGAGAAATCCAGATCAAGAGGATAGAGACCAAGACAAACAGCAAGTACGCTAT 61

Cy 22 SerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAspAla 41
Db 62 TCAAGAGAGAGAAATGGTTATTCAAGAAAGCAGCATGAGCTCAGGTTGTGTGAAGCT 121

Cy 42 LysValSerLeuLysLeuSerAsnThrAsnLysMetHisGluTyrIleSerProThr 61
Db 122 AGGGTTTCATTTCACTGTTCTCTACCTCCAAACAGCTTCATGAGTAAATCAGCCCTAAC 181

Cy 62 ThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyrArg 81
Db 182 ACCCAACAGAGAGAGATCGTAAATCTGTACCAAACTAATTTCTGAATGTGATGTTGGGCC 241

Cy 82 ThrHisGluGluSerMetLysAspThrLeuTyrPheLysGluIleAsnAsnLysLeu 101
Db 242 ACTCAATATATAGGAAATGCAGAGAAACAAAGAGAAATGTTGGACACAAATAGAAATTC 301

Cy 102 ArgArgGluIleArgGlnArgLeuGlnLysAspLeuAsnGlyLeuSerPheAspGluLeu 121
Db 302 CGAGCATCAGATCAAGCAGAGAGCTAGGTGAGTGTGGACGAGCTTGACATTCAAGAGACTG 361

Cy 122 AlaSerLeuAspArgGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
Db 362 CGTCGCTTATAGGATGAATGGAAAAACACTTTCAAACTCGTGTGGAGCGCAAGTTC 418

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Search completed: September 26, 2004, 11:29:32
Job time : 475.861 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 02:47:13; Search time 2630.89 Seconds
(without alignments)
2633.339 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARCKREKLIENTNQVT.....HGGSSGSSITLHDLRLA 232

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USFPO-SPool/US10069527/runat_23092004_163623_5752/app_query.fasta_1.782
-DB=EST -QFMT=fastap -SUFFIX=st -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10069527 @cgn 1.1.3596 @runat_23092004_163623_5752 -NCPU=6 -ICPU=3
-NO MAP -LARGOUPRY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELop=6 -DELext=7

Database :

EST:*
1: em.estba:*
2: em.esthum:*
3: em.estin:*
4: em.estm:*
5: em.estov:*
6: em.estpl:*
7: em.estro:*
8: em.hic:*
9: gb.est1:*
10: gb.est2:*
11: gb.hic:*
12: gb.est3:*
13: gb.est4:*
14: gb.est5:*
15: em.estfun:*
16: em.estom:*
17: em.gss.hum:*
18: em.gss.inv:*
19: em.gss.pln:*
20: em.gss.vit:*
21: em.gss.fun:*
22: em.gss.mam:*
23: em.gss.mus:*
24: em.gss.pro:*
25: em.gss.pig:*
26: em.gss.vit:*
27: em.gss.vit:*
28: gb.gss1:*

29: gb.gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	791.5	65.1	694	14	CB921382 VVD070D08
2	774.5	63.7	715	12	B1978526 ud03 Old
3	751	61.8	624	12	B1977629 jd10 Old
4	700.5	57.6	710	13	B0875031 V001F01 P
5	699.5	57.5	698	10	AW737915 EST339342
6	688.5	56.6	652	12	B1924444 EST54433
7	667.5	54.9	722	9	AJ559554 AJ559554
8	666.5	54.8	762	14	CB971393 CAB10005
9	666	54.8	697	9	AJ568191 AJ568191
10	652.5	53.7	757	13	B0877396 V033E07 P
11	652.5	53.7	727	14	AJ568207 AJ568207
12	651	53.5	727	14	CA990294 EST643802
13	646.5	53.2	800	9	AJ568199 AJ568199
14	646	53.1	692	14	CB972246 CAB10006
15	635.5	52.3	581	13	B0880121 B0880121
16	628.5	51.7	639	13	B0879075 V055E10 P
17	614	50.5	503	13	B0104750 B0104750
18	608	50.0	502	13	B0106725 fc1070.e
19	606	49.8	588	13	B0880503 B0880503
20	599.5	49.3	555	12	B1924402 CAB2S000
21	598.5	49.2	714	12	B1929568 EST549457
22	598	48.9	497	13	BQ104187 fc2185.e
23	595	48.9	590	10	AM624717 EST322662
24	581.5	47.8	590	12	B1928604 EST548693
25	580.5	47.7	605	12	B1928604 EST548693
26	580	47.7	573	12	B1928604 EST548693
27	580	47.7	575	12	B0559497 B0559497
28	565.5	46.5	623	10	AW944760 EST336810
29	563.5	46.3	576	12	B1929538 EST549427
30	560.5	46.1	567	10	AM624642 EST322587
31	560.5	46.1	717	14	CB838295 RFO2.110X
32	557.5	45.8	524	14	AM221174 EST297643
33	553.5	45.5	872	14	CD439730 EL01N0528
34	553.5	45.5	1273	11	AT109302 Zea mays
35	550	45.2	685	13	B0101040 QGJ12J06
36	549	45.1	508	13	B0878141 V043F04 P
37	549	45.1	678	9	A1485411 EST243732
38	549	45.1	670	9	A1485411 EST243732
39	542	44.6	543	12	B1928636 EST548525
40	541	44.5	532	12	B1930808 EST550797
41	540.5	44.4	642	14	CB087977 hK10F10.9
42	536.5	44.1	536	9	A1490575 EST249129
43	531	43.7	520	9	A1483797 EST249668
44	530.5	43.6	684	9	AJ559303 AJ559303
45	526	43.3	426	13	BQ106160 fc2475.e

ALIGNMENTS

RESULT 1
LOCUS CB921382
DEFINITION VVD070D08 353397 An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
ACCESSION CB921382
VERSION CB921382
KEYWORDS CDNA clone VVD070D08 5, mRNA sequence.
SOURCE
ORGANISM Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

US-10-069-527-4 (1-232) x B1978526 (1-715)

QY 1 MetAlaArgGlyLysIleGluIleLeuLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db ATGGGTCTGGGAGATTGAGATCAAGCTGATCGAAGACCAAGACGAGCAGGTACCC 120
 QY 21 TTTCTGATGAG 40
 Db TATTCGAGGAG 180
 QY 41 AAlaValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
 Db GCTCAGGCTCTCCCTCATCATGAGATCCCTCCATCGAAGAAATTCAGATATTAGCCCA 240
 QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
 Db ACCACTACGACCAAG 300
 QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
 Db AGCTACACCTACGAGGAG 360
 QY 101 LeuArgArgGluIleArgGlnArgLeuGlnLysHisAspLeuAsnGlyLeuSerPheAspGlu 120
 Db CTGAGGAGGAG 420
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 Db CTGCAAGATCTGAG 480
 QY 141 HisValIleLysThrGlnThrGlnThrLysLysLysValLysAsnLeuGluGlnArg 160
 Db CACGCTCTCAAG 540
 QY 161 ArgGlyAsn-MetLeuHisGlyTyrPheAspGlnGluAlaIleGlyLeuAspProGlnTyr 180
 Db AACAGTATTTTAAATGATGCTAT-----GAGAGCTCAGATATGAGATCCCAATA 594
 QY 180 GGLYTYRGLUASPANGLUGLYASPTYRGLUSERLALAEUSERANGLYALAAAS 200
 Db TGGGATGTGGATATGAAAGGAGCTATGATCTCTGCTTGGCAATGGAGCTCA 654
 QY 200 nasLeuTyrThrPhe-----HisLeuHisProAsnLeuHisHisGly 215
 Db 655 -AACTGATATTTTTCATCCGCTCCACACACACAACTTGTACCTGGAGCATGG 713
 QY 215 Y 215
 Db 714 G 714

RESULT 3
 LOCUS B1977629 624 bp mRNA linear EST 29-OCT-2002
 DEFINITION Jdo10 Old Blush petal SMART library Rosa chinensis cDNA 5' similar
 to APERAL3 (BnAP3), mRNA sequence.

ACCESSION B1977629
 VERSION B1977629.1 GI:24419435
 KEYWORDS EST.

SOURCE Rosa chinensis
 ORGANISM Rosa chinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosids; eucosids; I; Rosales; Rosaceae; Rosoideae; Rosa.
 REFERENCE 1 (bases 1 to 624)
 Chameliere,S., Riviere,S., Scalliet,G., Szecsi,J., Jullien,F.,
 Dolle,C., Vergne,P., Dumas,C., Bendahmane,M., Huguency,P. and
 Cock,J.M.

TITLE Analysis of gene expression in rose petals using expressed sequence
 tags
 JOURNAL FEBS Lett. 515 (1-3), 35-38 (2002)
 MEDLINE 21940574
 PUBMED 11943190

COMMENT

Contact: Cock JM
 RDP (UMR5667 INRA/CNRS/ENSL/UCBL)
 Ecole Normale Supérieure de Lyon
 46, Allée d'Italie, 69364 LYON Cedex 07, France
 Tel: 33472728611
 Fax: 33472728600
 Email: Mark.Cock@ens-lyon.fr
 PCR Primers
 FORWARD: CTCGGAGAGCGGCAATGTTGTTGTT
 BACKWARD: ATACGACTACATATGAGCGCAATTGGCC.

FEATURES

source
 Location/Qualifiers
 1..624
 /organism="Rosa chinensis"
 /mol_type="mRNA"
 /strain="Botanical garden, Lyon"
 /cultivar="Old Blush"
 /db_xref="taxon:74649"
 /dev_stage="Mixed (young bud, open bud, mature flower,
 senescing flower)"
 /lab_host="Escherichia coli"
 /clone_lib="Old Blush petal SMART library"
 /note="Organ: Petal; Vector: pTriblEx2; Site_1: Sfil;
 Site_2: Sfil"

ORIGIN

Alignment Scores:
 Pred. No.: 1,27e-71 Length: 624
 Score: 751.00 Matches: 142
 Percent Similarity: 84.82% Conservative: 20
 Best Local Similarity: 74.35% Mismatches: 27
 Query Match: 61.76% Indels: 2
 Gaps: 1

US-10-069-527-4 (1-232) x B1977629 (1-624)

QY 1 MetAlaArgGlyLysIleGluIleLeuLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db ATGGGTCTGGGAGATTGAGATCAAGCTGATCGAAGACCAAGACGAGCAGGTACCC 117
 QY 21 TTTCTGATGAG 40
 Db TATTCGAGGAG 177
 QY 41 AAlaValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
 Db GCTCAGGCTCTCCCTCATCATGAGATCCCTCCATCGAAGAAATTCAGATATTAGCCCA 237
 QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
 Db ACCACTACGACCAAG 297
 QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
 Db AGCTACACCTACGAGGAG 357
 QY 101 LeuArgArgGluIleArgGlnArgLeuGlnLysHisAspLeuAsnGlyLeuSerPheAspGlu 120
 Db CTGAGGAGGAG 417
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 Db CTGCAAGATCTGAG 477
 QY 141 HisValIleLysThrGlnThrGlnThrLysLysLysValLysAsnLeuGluGlnArg 160
 Db CACGCTCTCAAG 537
 QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleGlyLeuAspProGlnTyr 180
 Db AACAGTATTTTAAATGATGCTAT-----GAGAGCTCAGATATGAGATCCCAATA 591
 QY 181 GlyTyrGluAspAngluGlyAspTyrGlnLys 191

Db 592 GGGATATGATATGAAGGAGCTATGATCT 624

|||||

RESULT 4

LOCUS BUB75031 710 bp mRNA linear EST 16-OCT-2002

DEFINITION V001F01 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.

ACCESSION BUB75031

VERSION BUB75031.1 GI:24066555

KEYWORDS EST.

SOURCE

ORGANISM

Populus balsamifera subsp. trichocarpa (Populus trichocarpa)

Populus balsamifera subsp. trichocarpa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid 1; Malpighiales; Salicaceae; Salicaceae; Populus.

1 (bases 1 to 710)

Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.

The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries

Unpublished (2002)

CONTACT: BHALERAO RUPALI R.

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Department of Plant Physiology

University of Umea, 901 87 Umea, Sweden

Tel: +46 90 786 5279

Fax: +46 90 786 6576

Email: rupali.bhalerao@plantphys.umu.se.

Location/Qualifiers

1. 710

/organism="Populus balsamifera subsp. trichocarpa"

/mol_type="mRNA"

/sub_species="trichocarpa"

/db_xref="taxon:3694"

/tissue_type="floral buds"

/clone_id="Populus flower cDNA library"

/note="Organ: flower"

ORIGIN

Alignment Scores:

Pred. No.:	5.01e-66	Length:	710
Score:	700.50	Matches:	141
Percent Similarity:	76.64%	Conservative:	23
Best Local Similarity:	65.89%	Mismatches:	43
Query Match:	57.61%	Indels:	7
DB:	13	Gaps:	2

US-10-069-527-4 (1-232) x BUB75031 (1-710)

QY 1 MetAlaAGGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20

Db 85 ATGGCTGTGGAAAGATTGAATCAAGAAATGCAAAACCCCAACAGCGAAGTCACC 144

QY 21 TySerLysArgArgGlnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40

Db 145 TACCGAAGAGAAATGATATTTCACAAAGCCCAAGAACTCACTGACTTTGTGAT 204

QY 41 AlAlaValSerLeuIleMetLeuSerAsnThrAsnLysMetHisLysIleSerPro 60

Db 205 GCTTAGGCTCTCTTATCATGTTCTCCACACATCAACACTCAATAGATACATACCCC 264

QY 61 ThrThrThrThrLysSerMetCysAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80

Db 265 TCCACATCGAAGAAAGATCTACGATCATATCAAGACCTTACGATAGTCTGTGG 324

QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnLys 100

Db 325 GGCACCTCAATACGAAAGAAATGCAAGACCTTACGAGAGGTGAATATATCAATCAATAG 384

QY 101 LeuArgArgGlnIleArgGlnArgLysGlyHisAspLeuAsnGlyLeuSerPheAspGln 120

Db 385 CTGAGACAAAGAAATCAAGGAGAGAGAGAGAGAGGCTGATGATCTGAGCATTTGATCAT 444

QY 121 LeuAlaSerLeuAspAspGluMetGlnSerLeuAspAlaIleArgLysTyr 140

Db 445 CTGGCGGCTTGTACAAACATATGACTGAAGCTTGAATGTGTGCGTGGACGAAATGAC 504

QY 141 HisValIleLysThrGlnThrGluThrThrLysLysValLysAsnLeuGlnArg 160

Db 505 CATGTGATCAAAACCAAAACGAAACCTACAGAAAGAGGTGAAGATTTAGAGAGAGA 564

QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnIleAlaGlyGluAspProGlyTyr 180

Db 565 CATGAAACCTCTTATGGAATAT-----GAAAGAAACTTACAGAGATCGACAGTAT 615

QY 181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200

Db 616 GGTATTAGTGACAAAT-----GAACTGTGTGACCTTGCATTAATGGGCTTCC 663

QY 201 AsnLeuTyrThrPheHisLeuHisIleProAsnLeuHisHis 214

Db 664 AACCTTATGATTCGCTTCATCAACGAGCAACACACAC 705

RESULT 5

AW737915 698 bp mRNA linear EST 18-MAY-2001

LOCUS AW737915

DEFINITION EST339342 tomato flower buds, anthesis, Cornell University Lycopersicon esculentum cDNA clone CT04121 5', mRNA sequence.

ACCESSION AW737915

VERSION AW737915.1 GI:7646860

KEYWORDS EST.

SOURCE

LYCOPERSICON ESCULENTUM (tomato)

ORGANISM

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 698)

van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Roming, C.M., Nieman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

Generation of ESTs from tomato flower tissue, anthesis

Unpublished (1999)

CONTACT: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

Location/Qualifiers

1. 698

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultiivar="TA96"

/db_xref="taxon:4081"

/clone="CT04121"

/tissue_type="flower"

/dev_stage="anthesis"

/clone_id="tomato flower buds, anthesis, Cornell University"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA96). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

ORIGIN

Alignment Scores:

Pred. No.:	6.29e-66	Length:	698
Score:	699.50	Matches:	140
Percent Similarity:	72.84%	Conservative:	29
Best Local Similarity:	60.34%	Mismatches:	52
Query Match:	57.52%	Indels:	11
DB:	10	Gaps:	4

US-10-069-527-4 (1-232) x AW737915 (1-698)

Alignment Scores:

Pred. No.: 2,866-62 Length: 762
 Score: 666.50 Matches: 134
 Percent Similarity: 73.01% Conservative: 31
 Best Local Similarity: 59.29% Mismatches: 54
 Query Match: 54.81% Indels: 7
 DB: 14 Gaps: 3

US-10-069-527-4 (1-232) x CB971393 (1-762)

QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 10 ATGGCTAGAGGAAGATTGAGTCAAGAGATGAGAACTGACCAACAGGCAAGCTACCC 69
 QY 21 TySerIysArgGlnGlnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCyAsp 40
 Db 70 TACTCCAGAGACGAAATGATGATCTTCAAGAGCCGATGAGCTGCTGCTTGTGAT 129
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrlleSerPro 60
 Db 130 GCTAAGCTTTCTATCATCTGCTCTCCAGTACTGAGAAAGCTCCATGATACATCAAGCTT 189
 QY 61 ThrThrThrThrLysSerMetTyrlleAspAspTyrlleGlnLysThrMetGlyIleAspLeuTrp 80
 Db 190 TCCACTACACAGAAACAAATATTTGATCATGACCAAGAACTCTAGAGGATCTATGG 249
 QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTrpLysLeuGluIleAsnLys 100
 Db 250 AGCTTACCTATGAGAGATGCAAGAAACCTGAAAGAACTGAAAGATGCAAGAT 309
 QY 101 LeuArgArgGlnIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGln 120
 Db 310 CTCAGAGAGGAGATTAGGACAGAGATGGGTGAACATTGAGCGATTGAGCTTGAGGAA 369
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTrp 140
 Db 370 CTGCGAGATCTTGAAACAGAGATGAGAGATCTTGAAAGATGCTGAGATGAGAGATAC 429
 QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160
 Db 430 CAGGAGATCAATCAATCAATGAACTTCAAGAAAGATGAGAGATGAGAGATCAATA 489
 QY 161 ArgLysAsnMetLeuHisGlyTyrllePheAspGlnGlnAlaGlyLysAspProGlnTrp 180
 Db 490 CACAAATAATCTCTCATGAAATTT-----GATGACAGGACAGAGATCAATCTAT 540
 QY 181 GlyTyrlleAspAsnGluGlyAspTyrlleGlnSerAlaLeuAlaLeuSerAsnGlyValAsn 200
 Db 541 GGGCTAGTGCACATGAGGGGATTAAGAACTCTGCTTGGATTTCTCAATGAGAGCTCT 600
 QY 201 AsnLeuTyrllePheHisLeu-----HisHisProAsnLeuHisHisGlyLysSer 218
 Db 601 CCGGATATTGCCCTAAGCTTGAGAGCTTAACCGCTAATGATCTTCACTCGGGT----- 654
 QY 219 LeuGlySerSerIleThr 224
 Db 655 GTGGGCTCTGATTGACC 672
 RESULT 9
 AJ568191 697 bp mRNA linear EST 28-JUN-2003
 LOCUS AJ568191 Antirrhinum majus library (Stueber K) Antirrhinum majus
 DEFINITION cDNA clone zschol3a, mRNA sequence.
 ACCESSION AJ568191 GI:33294080
 VERSION AJ568191.1 GI:33294080
 KEYWORDS EST.
 SOURCE Antirrhinum majus (snaphdragon)
 ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Lamiales; Antirrhinaceae; Antirrhineae;
 Antirrhinum.
 REFERENCE 1 (bases 1 to 697)

AUTHORS Stueber, K. and Schwarz-Sommer, Z.
 TITLE Antirrhinum majus EST collection (Stueber, K. and Schwarz-Sommer, Z.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Stueber K
 Molecular Plant Genetics
 MPI fuer Zuechtungsforchung
 Carl-von-Linne Weg 10, D-50829, Germany.
 location/Qualifiers

FEATURES

source

1..697
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="zschol3a"
 /clone_lib="Antirrhinum majus library (Stueber K)"

ORIGIN

Alignment Scores:

Pred. No.: 2,866-62 Length: 697
 Score: 666.00 Matches: 126
 Percent Similarity: 73.30% Conservative: 36
 Best Local Similarity: 57.01% Mismatches: 53
 Query Match: 54.77% Indels: 6
 DB: 9 Gaps: 2

US-10-069-527-4 (1-232) x AJ568191 (1-697)

QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 38 ATGGCTAGAGGAAGATTGAGTCAAGAGATGAGAACTGACCAACAGGCAAGCTACCC 97
 QY 21 TySerIysArgGlnGlnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCyAsp 40
 Db 98 TACTCCAGAGAGAAATGATGATCTTCAAGAGCCGATGAGCTGCTGCTTGTGAT 157
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrlleSerPro 60
 Db 158 GCTAAGCTTTCTATCATCTGCTCTCCAGTACTGAGAAAGCTTCAAGATACATCAAGCTT 217
 QY 61 ThrThrThrThrLysSerMetTyrlleAspAspTyrlleGlnLysThrMetGlyIleAspLeuTrp 80
 Db 218 ACAAGTGCAGAAAGAGATGATGATCTGATCAAGAGAGCGCTGAGATGATCATGG 277
 QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTrpLysLeuGluIleAsnLys 100
 Db 278 AGCTTACCTATGAGAGATGCAAGAAACCTGAAAGAACTGAAAGATGCAAGAT 337
 QY 101 LeuArgArgGlnIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGln 120
 Db 338 CTCAGAGAGGAGATGACGAGAGATGGGTGAACATTGAGCGATTGAGCTTGAGGAA 397
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTrp 140
 Db 398 ATGTGAATCTTATGAAACATGAGATGATTAATCTCTCAAGCTCAATGTAAGAAAGTAC 457
 QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160
 Db 458 AAGATCATGATGACAGAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 517
 QY 161 ArgLysAsnMetLeuHisGlyTyrllePheAspGlnGlnAlaGlyLysAspProGlnTrp 180
 Db 518 CACAGAAAGCTGTG-----CTTGAATTTGATGACAGAGAGAGATCAACTTT 568
 QY 181 GlyTyrlleAspAsnGluGlyAspTyrlleGlnSerAlaLeuAlaLeuSerAsnGlyValAsn 200
 Db 569 GGATAGTGAATATAGAGGTGATTAATCTGCTTGGATTTCCCAATGAGAGGCTT 628
 QY 201 AsnLeuTyrllePheHisLeu-----HisHisProAsnLeuHisHisGlyLysSer 217
 Db 629 CGATATAGCCCTAAGAGCTCCGAGATCAATCAATCAATCAATCAATCAATCAATCAAT 688
 QY 218 Ser 218
 Db 689 TCT 691

RESULT 10
 BUS77396 605 bp mRNA linear EST 16-OCT-2002
 LOCUS BUS77396
 DEFINITION V033E07 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.
 ACCESSION BUS77396
 VERSION BUS77396.1 GI:24068920
 SOURCE EST.
 ORGANISM Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
 Populus balsamifera subsp. trichocarpa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 1 (bases 1 to 605)
 REFERENCE Umeberg, P., Bhalerao, R.R., Jansson, S. and Steirky, F.
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
 JOURNAL Unpublished (2002)
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@anphys.umu.se.
 FEATURES
 source
 1.605
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"
 /tissue_type="floral buds"
 /clone_id="Populus flower cDNA library"
 /note="Organ: flower"
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 Alignment Scores:
 Pred. No.: 7,01e-61 Length: 605
 Score: 652.50 Matches: 133
 Percent Similarity: 76.85% Conservative: 23
 Best Local Similarity: 65.52% Mismatches: 40
 Query Match: 53.66% Indels: 7
 DB: 13 Gaps: 2
 US-10-069-527-4 (1-232) x BUS77396 (1-605)
 QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 15 TTGGGTGCTGGAAGATTGCAATCAAGAGATCGAAACCCCAACAAGCGCATGACACC 74
 QY 21 TySerLysArgArgGlnGlyIlePheLysValAlaGlnGlnLeuThrValLeuCysAsp 40
 Db 75 TACTCGAAGAGAAATGGATTTTCAGAAAGCCCAAGACTCACTGACTTGTGAT 134
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 Db 135 GCTAAGGTCTCTTCATCATGTTCTCCACACTAACCAAACTCAATGATGATTAAGCCCC 194
 QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyLysAspLeuTyr 80
 Db 195 TCCAGCTCGAACAAGAGATCTAGATCAATATCAACAAGCGCTTAGGCTAGATCTGTGG 254
 QY 81 ArgThrHisGlnGlnSerMetLysAspThrLeuTyrLysLeuLysGlnIleAsnAsnLys 100
 Db 255 GGCAGCTCAATACGAGAAATGCAAGACACTTCAAGAGAGCTGATGATATCATCATCAAG 314
 QY 101 LeuArgArgGlnIleArgGlnArgLysIleAspLeuAsnGlyLeuSerPheAspGln 120
 Db 315 CTAGAGCAAGAAATCAAGCGAGAGAGAGAGGCGCTGATGATCTGAGCATTTGATCAT 374
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Db 375 CTGGCGGCTTGAGCAACATATGACTGAGCCTTGAAATGCTGTGCTGGCAGGAATGAC 434
 QY 141 HisValIleLysThrGlnThrGluThrThrLysLysValLysAsnLeuGlnArg 160
 Db 435 CATGTGATCAAAACCAAAAGCAACCTTCAAGAGAGAGGAGAAATTTAGAGAGAGA 494
 QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnIleAlaGlyGluAspProGlnTyr 180
 Db 495 CATGAAACCTCTTACAGGAATAT-----GAGCAAAACCTAGAGATCGACAGTAT 545
 QY 181 GlyTyrGluAspAsnGlnGlyAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 Db 546 GGTTTAGTG-----GACATTGAACCTGCTGTGACTTGCAATGCAAAATGGGGCTTCC 593
 QY 201 AsnLeuTyr 203
 Db 594 AACCTCAT 602
 RESULT 11
 AJ568207 757 bp mRNA linear EST 28-JUL-2003
 LOCUS AJ568207
 DEFINITION AJ568207 Antirrhinum majus library (Stueber K) Antirrhinum majus cDNA clone zschos3_7, mRNA sequence.
 ACCESSION AJ568207
 VERSION AJ568207.1 GI:33294096
 KEYWORDS EST.
 SOURCE Antirrhinum majus (snapdragon)
 ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Lamiales; Antirrhinaceae; Antirrhineae; Antirrhinum.
 1 (bases 1 to 757)
 REFERENCE Stueber, K. and Schwarz-Sommer, Z.
 TITLE Antirrhinum majus EST collection (Stueber, K. and Schwarz-Sommer, Z.)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Stueber K
 Molecular Plant Genetics
 MPI fuer Zuechtungsforchung
 Carl-von-Linne Weg 10, D-50829, Germany.
 Location/Qualifiers
 1.757
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
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 /clone="zschos3_7"
 /clone_id="Antirrhinum majus library (Stueber K)"
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 Alignment Scores:
 Pred. No.: 9.58e-61 Length: 757
 Score: 652.50 Matches: 126
 Percent Similarity: 72.65% Conservative: 36
 Best Local Similarity: 56.50% Mismatches: 54
 Query Match: 53.66% Indels: 7
 DB: 9 Gaps: 3
 US-10-069-527-4 (1-232) x AJ568207 (1-757)
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 QY 21 TySerLysArgArgGlnGlyIlePheLysValAlaGlnGlnLeuThrValLeuCysAsp 40
 Db 121 TACTCGAAGAGAAATGGTTTGCTCAAGAAAGACACAGAGCTCTGTTCTGTGAT 180
 QY 41 AlAlaValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnTyrIleSerPro 60
 Db 181 GCTAAGTTTCCATTATCATGATCTCAGATCTCAGAGCTTCACGATATCATCAGCCCA 240
 QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyLysAspLeuTyr 80

Db 241 ACAACTGGGACAAAGACGATTATTCATGATCATGAAAGCCGCTGGAGTTCATATG 300

Qy 81 AGTTHHISGLUGLISerMetLysAspThrLeuTTPlySLeuLysGLUILLAspAsnLys 100

Db 301 AGCTACACTATGAAATAATGCAGAGCACTTGAAGAAAGCTGATGAGTCAACGGAAT 360

Qy 101 LeuAAGATGGLUILLAspGlnArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGlu 120

Db 361 CTGAGAGGAGGAGATCAGGAAAGATGGGTGAGACTTGAACGATCGGCTACAGAA 420

Qy 121 LeuAAspLeuAspAspGlnMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140

Db 421 ATTGGAATCTTATGAAACATGATGATTAATCTTCAAGCTCATTCGTAAGAAAGATAC 480

Qy 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnGlnArg 160

Db 481 AAAGTCATCATGATACCATGATGCACACGAAAGAAAGTTAGAAATGTTGAAGAAATA 540

Qy 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGlnAlaIleArgLysAspProGlnTyr 180

Db 541 CACAGAAACCTGCTG-----CTTGAATTTGATGCAGAGAGAGAGATCCACACTTT 591

Qy 181 GLYTYRGLUAspAspGlnGlyAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200

Db 592 GGATTAGTTGATTAAGATGAAGTATTAATCTTCTCTGCTTCTCCAAATGAGAGGCT 651

Qy 201 AsnLeuTyrThrPheHisLeu-----HisHisProAsnLeuHisGly---Gly 216

Db 651 GGTATTAATGGCCCTACGCTCCCGACTATATCCATCTCTACTCTTCAAGAGGAAAGGCG 711

Qy 217 SerSerLeu 219

Db 712 TCTGATCTC 720

RESULT 12

LOCUS CA990294 727 bp mRNA linear EST 06-JAN-2003

DEFINITION EST143802 GESD Medicago truncatula cDNA clone GESD-28W21, mRNA

ACCESSION CA990294

VERSION CA990294.1 GI:27523188

KEYWORDS EST.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula

Medicago truncatula (barrel medic)

Burkhardt, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 727)

AUTHORS Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.

TITLE More ESTs from developing reproductive tissues of Medicago truncatula

JOURNAL Unpublished (2002)

COMMENT Contact: Grusak, M.A.

USDA/ARS Children's Nutrition Research Center

Baylor College of Medicine

1100 Bates Street, Houston, TX 77030-2600, USA

Tel: 713 798 7044

Fax: 713 798 7044

Email: mgrusak@bcm.tmc.edu

TIGR sequence name: MTPBS83TK

More information is available at: www.medicago.org

Seq primer: SKmod (CTA GAA GTA gAT CC).

FEATURES

source

1..727

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/mol_type="mRNA"

/cultivar="A17"

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/clone="GESD-28W21"

/issue_type="immature seeds"

/dev_stage="Immature seeds, 11 to 19 days after

pollination"

/clone.lib="GESD"

/note-Tvector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the UniZap XR vector from Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-2ap phage using Ex-assist helper phage and propagated in XL0R cells."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
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US-10-069-527-4 (1-232) x CA990294 (1-727)

Qy 1 MetAlaArgGlyLysIleGlnIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20

Db 13 ATGGCTGCTGTGAAGATGATGATTAAGTATGATGATGATGATGATGATGATGATGAT 72

Qy 21 TySerLysArgArgAsnGlyIlePheLysLysAlaGlnGlnLeuThrValLeuGlyAsp 40

Db 73 TACTCAAGAGAGAGATGATGATTAATCAAGAAAGACATCACTTGTCTTGTGAT 132

Qy 41 AlAlysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnTyrIleSerPro 60

Db 133 GCTAAGGTTTCATCATCATGATTTCTCCAAAATACAAAGATGATGATGATGATGATGAT 192

Qy 61 ThrThrThrThrLysSerMetLysAspAspTyrGlnLysThrMetGly---IleAspLeu 79

Db 193 GGTCTCTCAAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 252

Qy 80 ThrArgThrHisGlnGlnSerMetLysAspThrLeuTTPlySLeuLysGlnIleAsn 99

Db 253 TGGGTTCTCACTATGAAAGAAAGCTTGAAGAACTTGAAGAACTGAAAGATTAATTAACAT 312

Qy 100 LysLeuArgArgGlnIleArgGlnArgLeuGlnHis-----AspLeuAsnGlyLeu 116

Db 313 AAGCTTGAAGAGACGATCAGCATAGATAGATAGAGGAGGTGATGATGATGATGATGATGAT 372

Qy 117 SerPheAspGlnLeuAlaSerLeuAspAspGlnMetGlnSerSerLeuAspAlaIleArg 136

Db 373 AGCTTCAGCAAGCTGCTGATCTTGAAGAGATGATGATGATGATGATGATGATGATGATGAT 432

Qy 137 GlnArgSerTyrHisValIleLysThrGlnThrThrThrLysLysValLysAsn 156

Db 433 GAAAGAAAGTTTCATGATGATCAAAATCTCGACATGATCCGTGAGAAAGATTAAGAGC 492

Qy 157 LeuGlnGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGlnGlnAlaIleArg 176

Db 493 TTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543

Qy 177 AspProGlnTyrGlyTyrGlnAspAsnGlyLysTyrGlnSerAlaLeuAlaLeuSer 196

Db 544 CATTCAGATTTCTTTCACGAC--GAGAGAGAGAGAAATCAGACGTGCAATTCGCC 600

Qy 197 AsnGlyAlaAsnAsnLeuTyrThrPheHisLeuHisHisProAsnLeu----- 212

Db 601 AATGTCCTTCACTGATGATGATCTGTGACACCATCTCATCTGATGATGATGATGATGATGAT 660

Qy 213 HisHisGlyLysSerLeu 219

DB	661	CACCATGGAGAGAAAGTGA	681
RESULT 13			
LOCUS	AJ568199	800 bp	mRNA linear
DEFINITION	AJ568199 Antirrhinum majus library (Stueber K)	Antirrhinum majus	
ACCESSION	CDNA clone zsch022, mRNA sequence.		
VERSION	AJ568199		
KEYWORDS	AJ568199.1 GI:33294088		
SOURCE	EST.		
ORGANISM	Antirrhinum majus (snapdragon)		
REFERENCE	1 (bases 1 to 800)		
AUTHORS	Stueber, K. and Schwarz-Sommer, Z.		
TITLE	Antirrhinum majus EST collection (Stueber, K. and Schwarz-Sommer, Z.)		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Stueber K Molecular Plant Genetics MPI fuer Zuechtungsforchung Carl-von-Linne Weg 10, D-50829, Germany. Location/Qualifiers 1. 800 /organism="Antirrhinum majus" /mol_type="mRNA" /db_xref="taxon:4151" /clone="zsch022" /clone_idb="Antirrhinum majus library (Stueber K)"		
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Source			
Alignment Scores:			
Pred. No.:	4.68e-60	Length:	800
Score:	646.50	Matches:	127
Percent Similarity:	72.77%	Conservative:	36
Best Local Similarity:	56.70%	Mismatches:	53
Query Match:	53.17%	Indels:	8
Gaps:	9	Gaps:	3
US-10-069-527-4 (1-232) x AJ568199 (1-800)			
QY	1	Metlaaag-glylyysileglnllelyleuileglnbenglnthraanaaglnvalth	20
DB	61	ATGGCTCAGGGGAGGATCCAGATTAAAGATAGAGCAAAACAAAGGCGAGTAC	120
QY	20	rTysSerlysaArgaRgaenglyllePheLyblysaIaglnglnleuthrValleucysas	40
DB	121	CTACTCCAGAGAGAAATGGTTGTTCTCAGAAAGCACACGAGCTCTGTGTTCTGTGGA	180
QY	40	pAlalybAlseerleuileMeleuSerAsnthrasnlysmethisgilyrYlieserPr	60
DB	181	TGCTAAATTTCCATTATCATGATCTCCAGACTCAGAAAGCTTCACGAATCATCAGCCC	240
QY	60	oThrThrThrlyvssermetlyrAspAspTyrglnlysrhmctgylileaspleutr	80
DB	241	AACAACTCCGACAAAGCAGTATTCGATTCAGATTCAGAGGCGGTGAGTGTATCTATG	300
QY	80	pArgThrHisglnglnserMetlysaSpThrleuTrplysleuysglnileasnaAsnly	100
DB	301	GAGCTCACACATATGAGAAATATGCAAGACACTTGAAAGAGCTGATGAGCTCAACAGGA	360
QY	100	sleuAlaArglnuileargglnargyleuGlnHisaspLeuasnnglyleuSerpheaspl	120
DB	361	TCTGGAGGGGAGATCAGGCAAAAGATGGGAGAGCTTGAGACGATCGGGCTACGAACA	420
QY	120	uLeuAlasezLeuaspApjlnmetGlnserSerLeuaspAlaileargGlnArglysTy	140
DB	421	AATGTGATCTTATTGTAAGACATGAGATACTCTCTCAAGCTCATGTGTGAAGAAAGTA	480
QY	140	rHisVallelysrhmrglnhrnglnuthrThrlylelylelysalysaenleuGlnuGlnAr	160

DB	FEATURES	Source
Db	481 CAAAGTCATCAAGTAAACGATCGAACACGAGAGAAAAAGGTTAGAAATGTTGAAGAAAT	540
Qy	160 gAAGGlyAsmMetLeuHsHsGlyYrPheAspGlnGluAlaIaGlyGluAspProGlnTyr	180
Db	541 AACAGAAACCTGGG-----CTTGAATTTGATCAAGAGAGAGAGATCCACTT	591
Qy	180 TGLTYrGluAspAsnGlnGlyAspTYrGluSerAlaLeuAlaLeuSerAsnGlyAlaAs	200
Db	592 TGGATTAGTTATATATGAAGGTGATTTAATCTGCTCTGCTTCCCAATGAGAGGCC	651
Qy	200 nAsnLeuTYrThrPheHsSLeu-----HsHsProAsnLeuHsHsGly--G1	216
Db	652 TCGATATATGCGCCCTAGCGCTCCGAGTAACTAACACTTACTCTTCAACAGGAGAGGG	711
Qy	216 YSerSerLeu 219	
Db	712 CTCGATCTC 721	
RESULT 14		
LOCUS	CB972246	
DEFINITION	CB972246 692 bp mRNA linear EST 30-APR-2003	
ACCESSION	CAB10006.1a.Fa.D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 Vitis	
VERSION	vinifera_cDNA clone CAB10006.1a.Fa.D07 5', mRNA sequence.	
KEYWORDS	CB972246 CB972246.1 GI:30256403	
ORGANISM	EST, Vitis vinifera Vitis vinifera Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae; Vitaceae; Vitis. 1 (bases 1 to 692) Goes da Silva, F., Iandolino, A., Lim, H., Beek, J., Jones, K. and Cook, D. Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages Unpublished (2003) Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave, Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drc@ucdavis.edu Seq primer: ACGGTACCGACATATGCC. Location/Qualifiers 1..692 /organism="Vitis vinifera" /mol_type="mRNA" /culivar="Cabernet Sauvignon" /db_xref="taxon:29760" /clone="CAB10006.1a.Fa.D07" /sex="hermaphrodite" /dev_stage="Pre-bloom" /lab_host="DHSalpha" /clone_lib="Cabernet Sauvignon Flower Pre-bloom - CAB1" /note="Organ: Flower - Pre-bloom; Vector: pDNR; Site_1: Site_2: Still, CAB1 is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples were collected approximately eleven days before onset of bloom (clusters at this stage were fully developed and flowers with calyptaras or caps still attached. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5'-ATGACAGTGTATCAACGACAGATGCGCCATTACGCGCG-3' and 5'-ATTCAGAGCGCCGAGCGCGCCAGCAT-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 Kb size fraction."	

Pred. No.: 4,346-60 Length: 692
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 Percent Similarity: 73.15% Conservative: 28
 Best Local Similarity: 60.15% Mismatches: 52
 Query Match: 53.12% Indels: 6
 DB: 14 Gaps: 3

US-10-069-527-4 (1-232) x CB972246 (1-692)

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 QY 21 TysSerLyArgArgAsnGlyIlePheLySylsajIngluLeuThrValLeuCyasp 40
 Db 111 TACTCCAGAGACGAAATGCTATCTTCAAGAAAGCCATGAACTACCTGTTTGTGAT 170
 QY 41 AlAlysValSerLeuIleMetLeuSerAnThraenLyMetHisGlyTrIleSerPro 60
 Db 171 GCTAAGGTTTCTATCATGCTCTCCAGTACTGGAAGCTCCATGAAATCATCAGCCCT 230
 QY 61 ThrThrThrThrLysSerMetTyraSerPyrGlyIlySthMetGlyIleAspLeuThr 80
 Db 231 TCCACTACACGAAACAAATATTGTATCATGACGAAACACTGAGAGTGAGATCTATG 290
 QY 81 ArgThrHisGluGlySerMetLysAspThrLeuTrpLysLeuLySgluIleAspAsnLys 100
 Db 291 AGCTATCACTATGAGAGATGCAAGAAACCTGGAAGAACTGGAAGATGTAACAGAT 350
 QY 101 LeuAlaArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
 Db 351 CTCAGAAAGAGATTAAGGAGAGATGGGTGAACATTTGACGATTTAGGCTTGAGGAA 410
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTy 140
 Db 411 CTGGCAGATCTTGAACAGAGATGAGAGATTTTGAAGATGCTTCGAGAGAGAGATAC 470
 QY 141 HisValIleLysThrGlnThrGluThrLysLysLysValLysAsnLeuGlnArg 160
 Db 471 CAGGTGATCAATATCAATGAACTTGAACAAAGAAACGTAAGAGATGTGAACAAATA 530
 QY 161 ArgGlyAsnMetLeuHisGlyTyraPheAspGlnGluIleAlaGlyAspProGlnThr 180
 Db 531 CACAAAAATCTCTCATGAATTT-----GATGCAAGGAGACAGATCAATTTCTAT 581
 QY 181 GlyTyraGluAspAsnGluGlyAspTyraGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 Db 582 GGGCTAGTGAACAATGAGAGGGGATTAAGATCTGTTTGAATCTCAATGGAAGCTCT 641
 QY 201 AsnLeuTyraThrPheHisLeu-----HisHisProAsn---LeuHis 213
 Db 642 CCGGATTTGGCCCTAAGCTTGACGCTGAGACGCTTAATGATCTTTCAC 689

RESULT 15

BU880121 581 bp mRNA linear EST 16-OCT-2002

LOCUS BU880121 Populus flower cDNA library Populus balsamifera subsp.
 DEFINITION trichocarpa cDNA 5 prime, mRNA sequence.

ACCESSION BU880121 GI:24071645

VERSION BU880121.1

KEYWORDS EST.

SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)

ORGANISM Populus balsamifera subsp. trichocarpa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosid1; Malpighiales; Salicaceae; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 581)
 Unneberg, P., Bhaleero, R., Jansson, S. and Sterky, F.
 The Poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 Unpublished (2002)

JOURNAL CONTACT: BHALERAO RUPALI R.
 COMMENT Umea Plant Science Center

Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhaleero@plantphys.umu.se.
 Location/Qualifiers
 1. 581
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"
 /tissue_type="Floral buds"
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 /note="Organ: flower"

ORIGIN

Alignment Scores:

Pred. No.: 4,776-59 Length: 581
 Score: 635.50 Matches: 128
 Percent Similarity: 76.26% Conservative: 23
 Best Local Similarity: 64.65% Mismatches: 40
 Query Match: 52.26% Indels: 7
 DB: 13 Gaps: 2

US-10-069-527-4 (1-232) x BU880121 (1-581)

QY 12 GluAsnGlnThraSerArgGlnValThrTyraSerLyArgArgAsnGlyIlePheLysLys 31
 Db 4 AAAAAGCCCAAAACAGCAAGTCACTACTGCAAGAAAGAAATGATTTTCAAGAAA 63
 QY 32 AlGlnGlnLeuThrValLeuCyaspAlaLysValSerLeuIleMetLeuSerAnThr 51
 Db 64 GCCCAAGACTCACTGACTTGTGATGCTGAGAGTCTCTTATCATGTTCTCCACACT 123
 QY 52 AsnLysMetHisGlyTrIleSerProThrThrThrLysSerMetTyraSerPyr 71
 Db 124 AACAACTCAATGATGATCATTTAGCCCTCCATGCAACAAAGAAATGATCATAT 183
 QY 72 GlnLysThrMetGlyIleAspLeuTrpArgThrHisGluGlnSerMetLysAspThrLeu 91
 Db 184 CAGAACGCTTGAAGCTATGATCTGTGGGGCACTCAATACGAAATGCAAGAGCACTGT 243
 QY 92 TrpLysLeuLysGluIleAsnAsnLysLeuArgArgGluIleArgGlnArgLeuGlyHis 111
 Db 244 AGAAGCTGATATATATCAATCAATGAAGCTGAGCAAGAAATCGAGAGAGAGAGAG 303
 QY 112 AspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspAspGluMetGlnSer 131
 Db 304 GGCCTGATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
 QY 132 LeuAspAlaIleArgGlnArgLysValIleLysThrGlnThrGlnThrLys 151
 Db 364 TTGAATGGTGTGGTGGAGAGAGATGACATGTGATCAAAACAAACAAACCTTACAG 423
 QY 152 LysLysValLysAsnLeuGlnGlnArgArgGlyAsnMetLeuHisGlyTyraPheAspGln 171
 Db 424 AAGAGGTGAAGATTTAGAGAGACATGGAACCTCTGATGGAATTT----- 474
 QY 172 GluAlaAlaGlyGluAspProGlnTyraGlyTyraGluAspAsnGluGlyAspTyra 191
 Db 475 GAAGCAAAATAGAGATGACAGATGATGATGATGATGATGATGATGATGATGATG 522
 QY 192 AlaLeuAlaLeuSerAsnGlyAlaAsnAsnLeuTyraThrPheHisLeuHis 209
 Db 523 GCTGTGCACTTGCATAATGGGGCTTCAACCTTATGATCCGCTGCACTAC 576

Search completed: September 26, 2004, 07:03:49
 Job time: 2634.89 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 02:46:48 : Search time 361.219 Seconds
(without alignments)
2528.535 Million cell updates/sec

Title: US-10-069-527-2
Perfect score: 1103
Sequence: 1 MGRKVEIKRIENSNRQVT.....QQIPFAFRVQIPNIGERI 215

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 337863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO.spool/US10069527/runat.23092004.163623.5725/app.query.fasta_1.782
-DB=Geneseq.29Jan04 -QPM=fastap -SUFFIX=trng -MINMATCH=0.1 -ICORPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10069527 @CGN.1.1.586 @runat.23092004.163623.5725 -MCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq.29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	868	4	AAS00103
2	684.5	62.1	780	2	AAQ55089
3	660.5	59.9	896	9	ADDS5880
4	660.5	59.9	947	3	AAC39436
5	650	58.9	764	6	ABK82089
6	650	58.9	783	6	ABK82088
7	650	58.9	789	6	ABK82085
8	650	58.9	979	6	ABK82123

9	646	58.5	1065	6	ABK82124	Abk82086 Novel fllo
10	645	58.5	780	6	ABK82086	Abk82087 Novel fllo
11	645	58.5	783	6	ABK82087	Abk82087 Novel fllo
12	640	58.0	1065	6	ABK82127	Abk82127 DNA encod
13	639.5	58.0	1004	3	AAC46623	Aac46623 Zea may
14	632.5	57.3	909	3	AAC35208	Aac35208 Arabidops
15	623	56.5	1089	6	AAD42258	Aad42258 Corn Ap3
16	536	48.6	592	6	ABK82090	Abk82090 Novel fllo
17	398.5	36.1	1257	6	AAD42257	Aad42257 Corn Ap3
18	377.5	34.2	882	2	AAQ51189	AAQ51189 Homeotic
19	376	34.2	926	6	AAD42259	Aad42259 Soybean A
20	377	34.1	446	3	AAC48151	Aac48151 Zea may
21	358.5	32.5	989	3	AAC55879	Aac55879 Eucalyptu
22	358	32.5	681	4	AAFB5393	Aafb5393 Nucleotid
23	358	32.5	946	4	AAFB5392	Aafb5392 Nucleotid
24	358	32.5	946	4	ABK88485	Abk88485 Poplar pr
25	357.5	32.5	946	8	ACA62518	Aca62518 Poplar ho
26	357.5	32.4	959	3	AAC40831	Aac40831 Arabidops
27	356.5	32.3	954	3	AAC51525	Aac51525 Arabidops
28	356.5	32.3	1170	3	AAC51790	Aac51790 Arabidops
29	355.5	32.2	982	4	AAS00104	Aas00104 Granny Sm
30	354	32.1	954	3	AAC40685	Aac40685 Arabidops
31	353.5	32.0	1289	4	AAFB7549	Aafb7549 Rice MADS
32	352	31.9	924	3	AAFB7543	Aafb7543 Poplar fl
33	349.5	31.7	1250	4	AAFB5192	Aafb5192 Nucleotid
34	346	31.4	1342	2	AAFB9437	Aafb9437 Zea may
35	346	31.4	1345	2	AAFB58307	Aafb58307 Zea may
36	346	31.4	1345	2	AAFB6631	Aafb6631 APTM1A1
37	346	31.4	1345	2	AAFB6631	AAFB6631 Zea may
38	346	31.4	1345	2	AAFB6631	AAFB6631 Zea may
39	346	31.4	1345	2	AAFB6631	AAFB6631 Zea may
40	346	31.4	1345	3	AAFB6631	AAFB6631 Zea may
41	346	31.4	1345	3	AAFB6631	AAFB6631 Zea may
42	345.5	31.3	1239	3	AAFB6631	AAFB6631 Zea may
43	337	30.6	944	6	ABK82123	Abk82123 DNA encod
44	337	30.6	947	9	ABK82123	Abk82123 DNA encod
45	337	30.6	947	9	ABK82123	Abk82123 DNA encod

ALIGNMENTS

RESULT 1	AA00103	standard; CDNA; 868 BP.
ID	AA00103	standard; CDNA; 868 BP.
XX	AA00103;	
AC	AA00103;	
XX	AA00103;	
DT	11-SBP-2003	(revised)
DT	17-WAY-2001	(first entry)
XX	Granny Smith apple	CDNA encoding MdPI.
XX	Granny Smith apple	CDNA encoding MdPI.
XX	Granny Smith apple	CDNA encoding MdPI.
KW	Granny Smith apple; MdPI; seedless fruit; horticulture;	
KW	accelerated breeding programme; cross pollination; transgenic plant;	
KW	biennial bearing tendency; coding mech; ss.	
OS	Malus x domestica; var. Granny Smith.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..648
FT		/*tag= a
FT		/product= "MdPI"
FT	primer_bind	1..15
FT		/*tag= b
FT		/label= PCR_primer_p1_binding_site
FT	primer_bind	19..41
FT		/*tag= c
FT		/label= PCR_primer_p5_binding_site
FT	primer_bind	291..312
FT		/*tag= d
FT		/label= PCR_primer_p3_binding_site
FT	primer_bind	314..334
FT		/*tag= e

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FT primer_bind /tag= f
FT primer_bind /label= PCR primer p2_binding_site
FT primer_bind /tag= g
FT primer_bind /label= PCR primer p7_binding_site
FT primer_bind /tag= h
FT primer_bind /label= PCR primer p6_binding_site
PN M0200117334-A1.
XX 15-MAR-2001.
XX 07-SEP-2000; 2000WO-N2000176.
XX 07-SEP-1999; 99NZ-00337688.
XX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
XX Yao J, Morris BA;
XX MPI; 2001-235145/24.
XX P-PSDB; AA00186.
XX
XX New genetically modified fruiting plants that does not functionally
XX express MdPI or MdAP3 peptides, useful for producing seedless fruits,
XX specifically apple and its related species.
XX Claim 10; Fig 2; 41pp; English.
XX
XX The sequence encodes Granny Smith apple MdPI. The invention concerns a
XX fruiting plant that has been genetically modified so that it does not
XX functionally express the MdPI or MdAP3 peptide, producing seedless
XX fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3
XX may be used to transform fruiting plants, specifically apple and pear.
XX The polynucleotides may be used in modulating, reducing or eliminating
XX seed-bearing capacity in fruiting plants, used in horticulture, and in
XX breeding programmes to monitor the progress in breeding a stable seedless
XX fruiting plant. The polynucleotides may also be used in programmes for
XX identifying nucleic acid variants from fruiting plants. They can be used
XX for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
XX for use in an accelerated breeding programme to produce seedless fruit.
XX They may also be used in designing probes and primers for MdPI or MdAP3,
XX or their variants. The seedless fruiting plant is more convenient than
XX seeded fruit since these can be cropped without pollination, reducing
XX dependence on bees, pollinator varieties and warm weather at flowering.
XX The absence of pollen is also advantageous to alleviate environmental
XX concerns regarding the transfer of transgenes to non-transgenic by cross
XX pollination. Seedless cultivars can also avoid or reduce biennial bearing
XX tendencies that have been attributed to the inhibition of flower bud
XX formation by developing seeds and are less susceptible to codling moth
XX compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
XX field)
XX
XX SQ Sequence 868 BP, 296 A, 152 C, 208 G, 212 T, 0 U, 0 Other:
XX
XX Alignment Scores:
XX Pred. No.: 3,76e-105 Length: 868
XX Score: 1103.00 Matches: 215
XX Percent Similarity: 100.00% Conservativeness: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX Gaps: 0
XX
XX US-10-069-527-2 (1-215) x AA00103 (1-868)
XX
XX QY 1 MetG1AArgG1AysTAlaGluIleuYbArgG1IleGluAAsnSerSerAsnArgG1ValThr 20
XX Db 1 ATGGGACGTGGGAGGATTGATCAAGAGATTGAAGAACTCAAGTAAACGAGGACGAC 60
XX 21 TySerLysArgArgAsnG1IleIleIleTysLysAlaLysGluIleThrValLeuGlyasp 40

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Db 61 TACTCCAGAGGAGGAGATGGGATTATCAAGAGGCAAGAGATCTGTTCTATTTGAT 120
QY 41 AlAlaYalSerleullelleYrSerSerSergLYyMetValGluTYrCySerPro 60
Db 121 GCTAAGTATCTTTCATTTATTTCTAGCTCGGAGAGTGGTTGAATACAGCACCCCT 180
QY 61 SerThrThreuthrGluIleleuAaplyrTYrHiG1GlnSerL1yLysLysLeuTrp 80
Db 181 TCAACTACGCTGACAGAAATCTTGACCAATATACAGACATGACCAATCTGGAGAAATTGTGG 240
QY 81 AspAlaLysH1sgLubnsLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
Db 241 GATGCTTAGACATAGAAACCTCAGCAATGAGTGAATGATCAAGAAAGCATGACAC 300
QY 101 MetGlnValIleuLeuArgH1sleuLYsgLYIuAspIleThSerLeuAsnH1sValGlu 120
Db 301 ATGCAAGTAGAGCTCAAGCATCTGAAAGGAGAGACATCAACATGTAACCATGTAGAG 360
QY 121 LeuMetAlaleuGluGluIuAlaleuGluAsnG1YleuThSerL1eArgAspLYsgLnsEr 140
Db 361 CTGATGACCTTAGAGAGAGACCTTGAAATAGCCTTACAAAGTATCCGGGACAAAGCTCC 420
QY 141 LysEheValAspMetMetCargAspAsnG1YyAlaLeuGluAspGluAsnLYsATglu 160
Db 421 AAGTTCGTGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATTAAGCCCTC 480
QY 161 ThrTYrGluLeuGluInLYsgInGluInGluMetLYs11leLYsgLubnsValArgAsnMetGlu 180
Db 481 ACTTATAGCTGCAAAACCAACAGAGATGAAATTAAGAGANTGTGAAACATGGA 540
QY 181 AsnG1YrYrH1sgInArgGluInleuG1YAsnTYrAsnAsnAsnGlnGlnIn1leProPhe 200
Db 541 AATGGGATCATCATGAGAGGACGTGGGGAATCAACAAACACGACGAGATACCTTTT 600
QY 201 AlAphArgValGlnProIleGlnProAsnLeuG1uArgIle 215
Db 601 GCTTCGCGTGACGCTATTACGCCAATCTCAGAGAGATC 645

```

RESULT 2
AA05089 standard; cDNA; 780 BP.

AA05089;
16-OCT-2003 (revised)
25-MAR-2003 (revised)
25-JUN-1994 (first entry)

fbp1 cDNA for reverse genetic techniques.
XX flower; morphology; petals; MADS box protein; toxin gene; insect;
XX resistance; Frankliniella occidentalis; plant; ss.
XX Pecunia x hybrida.
XX

Key Location/Qualifiers
FT primer_bind 8..22
FT /tag= a
FT /note= "PCR primer"
FT primer_bind 731..753
FT /tag= b
FT /note= "PCR primer"

W09400582-A2.
XX 06-JAN-1994.
XX
XX 07-JUN-1993; 93WO-NL000121.
XX
XX 30-JUN-1992; 92EP-00201951.
XX (CPRO-) CPRO-DIO CENT PLANT BREEDING & REPRODUCT.

CC heat, cold, heavy metals, low light, drought, osmotic stress and salt
concentration). The present sequence is an environmental stress related
CC polynucleotide of the invention.

XX Sequence 896 BP, 285 A, 143 C, 218 G, 250 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	3,49e-59	Length:	896
Score:	660.50	Matches:	130
Percent Similarity:	75.81%	Conservative:	33
Best Local Similarity:	60.47%	Mismatches:	39
Query Match:	59.88%	Indels:	13
DB:	9	Gaps:	2

US-10-069-527-2 (1-215) x ADD55880 (1-896)

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QY      1 MetGlyArgGlyLysValGluIleLysArgGluAsnSerSerAspArgGluValThr 20
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QY      21 TyrSerLysArgArgAsnGlyIleIleLysLysAlaLysGluIleThrValLeuGlyAsp 40
DB      84 TTCTCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 143
QY      41 AlaLysValSerIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 60
DB      144 GCAAGAGTCCCTCAATCTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 203
QY      61 SerThrThrLeuThrGluIleLeuAspLysLysArgGlySerGlyLysLysLysLeuTrp 80
DB      204 TCATATGATCTTGGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 263
QY      81 AspAlaLysHisGluLeuLeuSerAsnGluValAspArgValLysLysAspAspSer 100
DB      264 GATGCTAAGAGATAGAACCTTACCAATGATGATGATGATGATGATGATGATGATGATGAT 323
QY      101 MetGluValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
DB      324 TTCAATGAGAGCTTCAGCATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
QY      121 LeuMetAlaLeuGluGluIleValLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
DB      384 CTATGAGCTGTCAGAGACCGCATTTGAAACATGCGCTCGACAAAGTCCGAGACCAACAGATG 443
QY      141 LysPheValAspMetLeuArgAspAsnGlyLysAlaLeuGluAsnGluAsnLysArgLeu 160
DB      444 GAGATCTTATATCAAGAGAGAGAGAGAGAGAGATGAGAGATGAGAGAGAGAGAGAGATG 503
QY      161 ThrTyrGluLeuGlnLysGlnGlnIleMetLysIleLysGluAsnValArgAsnMetGlu 180
DB      504 ACTTTCAGCTGCA---CAACAGAGATGCGTATGCAAGCAACGACAGAGATGATG 560
QY      181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnIleLeuPhe 200
DB      561 ATGAGAGATCATATGAGGAG-----TTT 584
QY      201 AlaPheArgValGlnProIleGlnProAsnLeuGlnIleArgIle 215
DB      585 GGAATATGAGTGCACCGATTCAGCAATCTTCAAGAAAGATT 629
RESULT 4
AAC39436
ID AAC39436 standard; DNA; 947 BP.
XX
AC AAC39436;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24624.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KM promoter; termination sequence; ss.
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XX OS Arabidopsis thaliana.
XX XX
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 3,74e-59 Length: 947
Score: 660.50 Matches: 130
Percent Similarity: 75.81% Conservative: 33
Best Local Similarity: 60.47% Mismatches: 39
Query Match: 59.88% Indels: 13
DB: 3 Gaps: 2

US-10-069-527-2 (1-215) x AAC39436 (1-947)

QY 1 MetGlyARGLylyValGluIlelySArgIIeGIuAnSerSerAsnArgGlnValThr 20
DB 122 ATGGGTAGAGAGAAAGTCAGATTAAGAGATAGAGAACGAAACAGAGAGTGTGAG 181

QY 21 TyrSerLyARkARsngIlyleIlelySAlaLySGIuIleThrValLeuCyAsp 40
DB 182 TTCTCAAGAGAGAGATTCGATTCGAGAGAGCTTAAGAAATACAGATTCTTGTGAT 241

QY 41 AlaLyValSerLeuIleIleTyrSerSerSergLyLysMetValGluTyrCySerP 60
DB 242 GCAAAAGTTCCTCATTAATCTTCAGAGTAATGTAAGATGATGATTAATGTTGCTCT 301

QY 61 SerThrThrLeuThrGluIleLeuAspLyTyRHISGlyGlnSerGlyLysLeuTyr 80
DB 302 TCCATGATCTTGCTGCTTGTGAGCCAAATCCAGAACTTATTCGCAAGAACTAAG 361

QY 81 AspAlaLyHISGlyuAnSerSerSergIuValAspArgValLySAspAsnAspSer 100
DB 362 GATGCTAAGATGAGAACTTGAATGATGATGATGATGATGATGATGATGATGATG 421

QY 101 MetGluValGluLeuArgHisLeuLysGluValAspIleThrSerLeuAsnHisValGlu 120
DB 422 TTTCACTGAGAGCTCAGGCTTTGAAAGGAGAAATATACAGTCTTCAACTTGAATAAT 481
QY 121 LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
DB 482 CTATGAGCTGCTCAGAGCAAGCCATTGAAACATGGCTCGAACAAGTCCGAAACACCAAGAGATG 541
QY 141 LysPheValAspMetLeuArgAspAsnGlyValAlaLeuGluAspLysAsnHisValGlu 160
DB 542 GAGATCTTATATCAAAAGAGAGAAATGAGAAATGATGATGCGGAGGAGCAAGCAATC 601
QY 161 ThrTyroGluLeuGluLysGlnGlnGlnGlnMetLysIleLysGluAsnValArgAsnMetGlu 180
DB 602 ACTTCCAGCTGCA---CAACAGAGATGGCTATGACAGCAAGCAAGCAAGAGATGATG 658
QY 181 AsnGlyTyroHisGluArgGlnLeuGlyAsnTyroAsnAsnAsnGlnGlnIleProPhe 200
DB 659 ATGAGAGATCATGATGAGGAG---TTT 682
QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle 215
DB 683 GATATATGAGTGCACCGATTCAGCCAAATCTTACAGAAAGATT 727
RESULT 5
ABK82089 standard; cDNA; 764 BP.
XX
AC ABK82089;
XX
DT 27-AUG-2002 (first entry)
XX
DE Novel floral meristem identity gene LpMADS1 contig #4.
XX
XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
KM CEN-like protein; APERIALA2; AP2; AP2-like protein; HB; Homeo-box protein;
KM HB-like protein; plant growth; plant architecture;
KM Inflorescence development; flower development; embryo development;
KM seed development; flower organ identity; phase change; male sterility;
KM hybrid seed production; herbage quality; early maturing crop;
KM biomass increase; branching increase; blocking flowering;
KM allergenic pollen; floral meristem identity protein; ss.
XX
OS Lolium perenne.
XX
PN W0200233091-A1.
XX
PD 25-APR-2002.
XX
PF 17-OCT-2001; 2001WO-AU001311.
XX
PR 19-OCT-2000; 2000AU-00000873.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PI Spangenberg G, Sawbridge TJ, Ong EK, Emmerling M;
XX WPI; 2002-454601/48.
XX
PT New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APERIALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.
XX
PS Claim 3; Fig 29; 290pp; English.
XX
CC The invention describes a substantially purified or isolated polypeptide
CC (1) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, APERIALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.

CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases: flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced bushiness in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles
XX
SQ Sequence 764 BP; 225 A; 202 C; 206 G; 129 T; 0 U; 2 Other;
XX
Alignment Scores:
Pred. NO.: 3.52e-58 Length: 764
Score: 650.00 Matches: 122
Percent Similarity: 77.00% Conservative: 42
Best Local Similarity: 57.28% Mismatches: 43
Query Match: 58.93% Indels: 6
DB: Gaps: 2
US-10-069-527-2 (1-215) x ABK82089 (1-764)
QY 1 MetGluValGluLeuArgHisLeuLysGluValAspIleThrSerLeuAsnHisValGlu 20
DB 84 ATGGGGGCGGAGAGATCGATCAAGAGATGAGAGAACCGAGCAAGCGCGAGTACC 143
QY 21 TyroSerLysArgArgAsnGlyIleIleLysValAlaLysGluIleThrValLeuCyAsp 40
DB 144 TTCTCCAAAGCGCAAGAACGGGATCTCTCAAGAGCCAGAGATGACGCGTCTCGAC 203
QY 41 AlaLysValSerLeuIleIleTyroSerSerGlyLysMetValGluTyroCySerPro 60
DB 204 GCCGAGGTCCGCGTCCGCTCTCTCCAGCGCGGCAAGCTCTACACCTTCTGCTCCCC 263
QY 61 SerThrThrLeuThrGluIleLeuAspLysTyroHisGlyLysSerGlyLysLysLeuTrp 80
DB 264 AAGCATCGCTATCAAGATCTTGGAGATGATCCAGACCACTCCGGGAAGATCTGTGG 323
QY 81 AspAlaLysHisGluLeuLeuSerAsnGlyValAlaAspArgValLysLysAspAsnAspSer 100
DB 324 GATGAGAAACAAAGAGCTCAGCGCGGAGATGATGATGATCAAGAAAGAAATGATTAAC 383
QY 101 MetGluValGluLeuArgHisLeuLysGluValAspIleThrSerLeuAsnHisValGlu 120
DB 384 ATGCAAGATGAGAGCTCAGGCACTTGAAGAGGAGAAATCTGACTCTGCAACCAAGAG 443
QY 121 LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
DB 444 TTGATCATGATGAGGAGACATGATTAATGAGCTACAGGCTCGATGATGAAAAAGATG 503
QY 141 LysPheValAspMetLeuArgAspAsnGlyValAlaLeuGluAspLysAsnHisValGlu 160
DB 504 GAGACATCAACAGCGCTGATGAAACTGCGAAGATCTGAAAGATGAAACAAAGTTGCTC 563
QY 161 ThrTyroGluLeuGlnGlnGlnGlnMetLysIleLysGluAsnValArgAsnMetGlu 180
DB 564 GATTTAAATCGAT---CAGCAAGATATTCGCTGTAAGGAGCAATGAGGAGCTTGA 620

XX DNA encoding novel floral meristem identity protein *lpmADS1*.
 DE Ryegrass; fecuene; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 XX CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KM HB-like protein; plant growth; plant architecture; HB; Homeo-box protein;
 KM inflorescence development; flower development; embryo development;
 KM seed development; flower organ identity; phase change; male sterility;
 KM hybrid seed production; herbage quality; early maturing crop;
 KM biomass increase; branching increase; blocking flowering;
 KM allergenic pollen; floral meristem identity protein; gene; ss.
 OS *Lolium perenne*.
 XX MO200233091-A1.
 XX 25-APR-2002.
 PD 17-OCT-2001; 2001MO-AU001311.
 XX 19-OCT-2000; 2000AU-00000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRSEARCH LTD.
 XX Spangenberg G, Sawbridge TJ, Ong EK, Emmerling M;
 PI WPI: 2002-454501/48.
 DR P-PSDB: ABG60932.
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 PS Claim 3, Fig 27, 290pp; English.
 XX The invention describes a substantially purified or isolated polypeptide
 CC (1) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB),
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles
 XX Sequence 789 BP; 233 A; 207 C; 211 G; 138 T; 0 U; 0 Other.

Alignment Scores: 3.67e-58 Length: 789
 Pred. No.: 650.00 Matches: 122
 Score:

Percent Similarity: 77.00% Conservative: 42
 Best Local Similarity: 57.28% Mismatches: 43
 Query Match: 58.93% Indels: 6
 DB: 6 Gaps: 2
 US-10-069-527-2 (1-215) x ABK82085 (1-789)
 QY 1 MetGlyArgGlyValValGluIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 20
 DB ATGGGGCGCGGAGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 143
 QY 21 TyrSerLysArgGlyValValGluIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 40
 DB TTCTCCAGGCGGAGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 203
 QY 41 AlaLysValSerLeuIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 60
 DB GCGGAGGCGGCGGAGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 263
 QY 61 SerThrThrLeuThrGluIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 80
 DB 264 AAGACATCGCTTATCAAGATCTTGAGAGATCGATCGATCGATCGATCGATCGATCGATCGATCG 323
 QY 81 AspAlaLysSerLeuIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 100
 DB 324 GATGAGAAACACAGAGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 383
 QY 101 MetGlnValGluLeuValArgIleGluAsnSerSerAsnArgGlnValThr 120
 DB 384 ATGCAGATCGGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 443
 QY 121 LeuValLeuGluGluIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 140
 DB 444 TTGATCATGATGAGAGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 503
 QY 141 LysPheValAspMetLeuValArgIleGluAsnSerSerAsnArgGlnValThr 160
 DB 504 GAGCAGTACAGCAGGCTGATGATAAACTGCAAGATCGATGATGATGATGATGATGATGATGATGATG 563
 QY 161 ThrThrLeuGluGluIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 180
 DB 564 GCATTAACTGCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 620
 QY 181 AsnGlyThrIleGluGluIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 200
 DB 621 CTGCTTACCATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 665
 QY 201 AlaPheValGluGluIleLeuValArgIleGluAsnSerSerAsnArgGlnValThr 213
 DB 666 ACGTTCCGCGTGGAGCTTACCAACCCCAACCTGACAGAG 704
 RESULT 8
 ID ABK82123 standard; cDNA, 979 BP.
 AC ABK82123;
 XX 27-AUG-2002 (first entry)
 DE DNA encoding novel floral meristem identity protein *lpmADS1*.
 KM Ryegrass; fecuene; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KM CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KM HB-like protein; plant growth; plant architecture;
 KM inflorescence development; flower development; embryo development;
 KM seed development; flower organ identity; phase change; male sterility;
 KM hybrid seed production; herbage quality; early maturing crop;
 KM biomass increase; branching increase; blocking flowering;
 KM allergenic pollen; floral meristem identity protein; gene; ss.
 OS *Lolium perenne*.
 XX MO200233091-A1.

XX 25-APR-2002.
 PD 17-OCT-2001; 2001MO-AU001311.
 XX 19-OCT-2000; 2000AU-00000873.
 PR (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRSEARCH LTD.
 PA Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PT WPI; 2002-454601/48.
 DR P-PSDB; ABG60941.
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 XX Claim 3; Fig 54; 290pp; English.
 PS
 XX The invention describes a substantially purified or isolated polypeptide
 CC (i) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (ii) encoding (i), a construct (iii) comprising (ii), or a
 CC vector (iv) comprising (ii), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (ii), (iii) or (iv) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles
 CC
 CC SQ Sequence 979 BP; 305 A; 236 C; 246 G; 192 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 4.8e-58 Length: 979
 Score: 650.00 Matches: 122
 Percent Similarity: 77.00% Conservative: 42
 Best Local Similarity: 57.28% Mismatches: 43
 Query Match: 58.93% Indels: 6
 DB: Gaps: 2
 US-10-069-527-2 (1-215) x ABK82123 (1-979)
 QY 1 MetGtYAArGtGtYtValGtUtleYsArGtJleGtUaSenSerSArSArGtUValThr 20
 DB 134 ATGGGGCGCGGGAAGATCGAGTCAAGAGATCGAAGACCGAGAAACCGCAGGTGACC 193
 QY 21 TYSerLYsArGtArGtAsnGtYlleTleYsLYsAlaLYsGtUleThrValleuCYsAsp 40
 DB 194 TTCTCCAAGCGCAAGACCGGATCTCTCAAGAAAGCCCAAGAGATCAGGTGCTGTGCAC 253

QY 41 AlalysValSerLeuIleIleTyrSerSerSerGtLYsMetValGtUtyCYsSerPro 60
 DB 254 GCCGAGGTGCGGCGTGTGCTCTTCCAGCCCGGACGCTCTACGACTTGTGCTCCCC 313
 QY 61 SerThrThrLeuThrGtUtleYsAspLYsTyrHisGtYnsSerGtLYsLYsLeuTyr 80
 DB 314 AAGACATGCTATCAAGATCTTGGAGAGATCCAGACCACTCCGGGAAATACTGTGG 373
 QY 81 AspaLYsSHIsgUaSnLeuSerAsnGtUValAspaLYsLYsAspaSnAspSer 100
 DB 374 GATGAGAAACCAAGACCTCAGCGCGGAGATTGATCAATCAAGAAAGAAATGATAC 433
 QY 101 MetGtUValGtUleuArGtHisLeuLYsGtYnAspIleThrSerLeuAsnHisValGtU 120
 DB 434 ATGCAGATCGAGCTCAGGACTTGAAGCGAAGATCTGAATCTCCTCAACCCAAAG 493
 QY 121 LeuMetAlaLeuGtUValAlaLeuGtUAsnGtYnSerIleArGtAspLYsGtYnSer 140
 DB 494 TTGATCATGATTGAGGAAGCACTTATATGACTGACAGGCTGTCAGAAACAGATG 553
 QY 141 LysPheValAspMetMetArGtAspAsnGtLYsAlaLeuGtUAspGtUAsnLYsArGtU 160
 DB 554 GAGCACTACGACAGGCTGATGAAACTGGCAAGATGTAGAGATGAAACAAAGTTGCTC 613
 QY 161 ThrTYrGtUleuGtUleuGtUleuGtUleuTyrHisGtYnAsnValArGtAsnMetGtU 180
 DB 614 GCATTTAACCTGCA---CAGCAAGATTTGGCGCTGAACGGGAATATGGAGAGCTTAG 670
 QY 181 AsnGtYTYrHisGtUArGtUleuGtUAsnTYrAsnAsnAsnGtUleuGtUleuProhe 200
 DB 671 CTGGTTCATCCATCCGACAGG-----GACTTGCAGCCCAATGCCGATC 715
 QY 201 AlaPheArGtValGtUProIleGtUProAsnLeuGtUleu 213
 DB 716 AGCTTCGCTGCAAGCTTACCCACCCCAACTGCGAGAG 754
 RESULT 9
 ID ABK82124 standard; cDNA; 1065 BP.
 XX ABK82124;
 AC
 XX
 XX 27-AUG-2002 (first entry)
 DT
 XX
 DE DNA encoding novel floral meristem identity protein LpMADS1b.
 KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; gene; ss.
 KW
 XX
 XX Lolium perenne.
 OS
 XX
 XX WO200233091-A1.
 PN
 XX
 PD 25-APR-2002.
 XX
 PF 17-OCT-2001; 2001MO-AU001311.
 XX
 PR 19-OCT-2000; 2000AU-00000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRSEARCH LTD.
 PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 DR WPI; 2002-454601/48.
 DR P-PSDB; ABG60941.
 XX

CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced biomass in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles
XX
SQ Sequence 780 BP, 229 A; 203 C; 206 G; 136 T; 0 U; 6 Other;

Alignment Scores:

Pred. No.: 1,2e-57 Length: 780
Score: 645.00 Matches: 122
Percent Similarity: 76.53% Conservative: 41
Best Local Similarity: 57.28% Mismatches: 44
Query Match: 58.48% Indels: 6
DB: Gaps: 2

US-10-069-527-2 (1-215) x ABK82086 (1-780)

QY 1 MetGlyArgGlyValGluIleValArgIleGluAsnSerSerAsnArgIleValThr 20
DB 84 ATGGGGCGGTGGAGAGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 143
QY 21 TySerIysArgArgAsnGlyIleIleValAlaValGlySerIleThrValLeuCyAsp 40
DB 144 TTCTCCAAAGCGCAAGAGCGGATCTCCAGAGCGCAAGAGATCGATCGATCGATCG 203
QY 41 AlaIysValSerIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 60
DB 204 GCCAGGATCGCGCGTCTCTCTCCAGCGCGCGGAGGATCGATCGATCGATCGATCG 263
QY 61 SerThrThrLeuThrGluIleLeuAspIleTyThrIleGlyIleSerGlyIleValLeuTrp 80
DB 264 AAGCAATCGCTATCAAGATCTTGAGATCGATCGATCGATCGATCGATCGATCGATCG 323
QY 81 AspAlaIysHisGluAsnLeuSerAsnGluValAspArgValIleIleIleIleIleIleIle 100
DB 324 GATAGAGAAACACAGAGCTTCAGTCCGAGATTCATCAATCAAGAAAGAAATGACAC 383
QY 101 MetGluValGluLeuValGlyIleValGlyIleValGlyIleValGlyIleValGlyIle 120
DB 384 ATGCAAGATCGAGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTC 443
QY 121 LeuMetAlaLeuGluGluIleValGluAsnGlyIleThrSerIleArgAspIleGlnSer 140
DB 444 TTGATCATGATTGAGAGACCTTGATATGAGATCGATCGATCGATCGATCGATCGATCG 503
QY 141 LysIleValAlaMetMetArgAspAsnGlyValAlaLeuGluValAspGluValAspGlu 160
DB 504 GAGCACTACGACAGCGCTGATGAAAATCGGCAAGTCTAGAGATGAGAAACAGATGCTC 563
QY 161 ThrTyrgluLeuGlnIleValGlnIleValGlnIleValGlnIleValGlnIleValGln 180
DB 564 GCATCTAACTGCAT---CAGCAAGATATTCGCTGAACGGGAAATCAAGAGGAGCTTGAG 620
QY 181 AsnGlyIleValGlnIleValGlnIleValGlnIleValGlnIleValGlnIleValGln 200
DB 621 CTTGGTAACTACCGGACAGG-----GACCTTGACCGCCAGATGCGCATC 665

QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnIle 213
DB 666 ACGTTCGCGTGGACGCTAGCCAGCACCCCACTGGAGGAG 704
RESULT 11
ABK82087
ID ABK82087 standard; cDNA, 783 BP.
AC ABK82087;
XX
XX 27-AUG-2002 (first entry)
DE Novel floral meristem identity gene LpMADS1 contig #2.
KM Ryegrass; fescue; MADS-box; MADS; AP2-like protein; CENTRORADIALIS; CEN;
KM CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
KM HB-like protein; plant growth; plant architecture;
KM inflorescence development; flower development; embryo development;
KM seed development; flower organ identity; phase change; male sterility;
KM hybrid seed production; herbage quality; early maturing crop;
KM biomass increase; branching increase; blocking flowering;
KM allergenic pollen; floral meristem identity protein; ss.
XX
XX Lolium perenne.
OS
XX
XX WO200233091-A1.
XX
XX 25-APR-2002.
XX
XX 17-OCT-2001; 2001WO-AU001311.
XX
XX 19-OCT-2000; 2000AU-00000873.
XX
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRISearch LTD.
XX
XX Spangenberg G. Sawbridge TI, Ong EK, Emmerling M;
PI WPI; 2002-454601/48.
XX
XX New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.
XX
XX Claim 3; Fig 29; 290pp; English.

The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;

CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a coding
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles
XX
SQ Sequence 783 BP; 233 A; 204 C; 208 G; 136 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 1.2e-57 Length: 783
Score: 645.00 Matches: 122
Percent Similarity: 76.53% Conservative: 41
Best Local Similarity: 57.28% Mismatches: 44
Query Match: 58.48% Indels: 6
DB: 6 Gaps: 2

US-10-069-527-2 (1-215) x ABK82087 (1-783)

QY 1 MetGlyArgGlyValGluIleTyrSerSerSerGlyValMetValGluTyrCysSerPro 20
DB 82 ATGGGGCGTGGAGATCGATCAAGAGATGAGAACCAAGCAACCCAGGTGACC 141
QY 21 TyrSerIleArgArgAngIleIleIleValAlaIleGluIleThrValIleuGlyAsp 40
DB 142 TTCTCCAGCGCAAGACGGGATCTCTCAAGAGCGCAAGAGATGAGCTGCTGCGAC 201
QY 41 AlaIleValSerIleIleTyrSerSerSerGlyValMetValGluTyrCysSerPro 60
DB 202 GCGGAGTCCGCTGCTGCTCTCTCCAGGCGGCAAGCTGACACTTCTGCTCCCA 261
QY 61 SerThrThrLeuThrGluIleLeuAspIleTyrHisGlyIleSerGlyIleuGlySer 80
DB 262 AAGACATCGCTATCAAGAAATCTTGAGAGATACCAAGCAACCTCCGAGAGATCTGTG 321
QY 81 AspAlaIleHisGluIleuSerSerSerGluValAspArgValIleValAspAsnSer 100
DB 322 GAAGAGAAACAGAGCTCAGTCCGAGATGATGATCAAGAAAGAAATACACAC 381
QY 101 MetGluValGluIleuArgHisLeuIleGlyIleuAspIleThrSerLeuAsnHisValGlu 120
DB 382 ATCCAGATCGAGCTGAGCGACTTGAGAGGAGAGATCTCACTCACTGCAACCCAAAG 441
QY 121 LeuMetAlaIleuGluIleuAlaIleuGluIleuThrSerIleArgAspIleuSer 140
DB 442 TTATATATGATGATGAGAGCACTTGATGATGCTACAGCGCTGATGATGATGATG 501
QY 141 LysPheValAspMetLeuArgAspAsnGlyValAlaIleuGluAspGluAsnIleuSer 160
DB 502 GAGCACTAGCAGCAGCTGATGAAAAGCTGCAAGATCTGAGAGATGAGAAAGTTGCTC 561
QY 161 ThrTyrGluIleuGluIleuGluIleuMetValIleValGluAsnValArgAsnMetGlu 180
DB 562 GCATCTAAACTGCAT---CAGCAAGATATTGGCTGAGAGGAGAAATGAGAGCTTGA 618
QY 181 AsnGlyTyrHisGluIleuArgIleuGluIleuYasnAsnAsnGluIleuProhe 200
DB 619 CTGGTTACCATCCGACAGG-----GACTTTGACAGCCCATGATGCGCATC 663
QY 201 AlaPheArgValGluIleuProIleuProAsnIleuGluIleu 213
DB 664 ACCTTCGCGTGAAGCTAGCAACCCAGCTGAGAG 702
RESULT 12
ABK82127
ID ABK82127 standard; cDNA; 1065 BP.
XX
AC ABK82127;
XX
DT 27-AUG-2002 (first entry)
XX
DE DNA encoding novel floral meristem identity protein LpMADS2-3.
XX
KM Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;

KM CEN-like protein, APTAL2, AP2, AP2-like protein; HB; Homeo-box protein;
KM HB-like protein; plant growth; plant architecture;
KM inflorescence development; flower development; embryo development;
KM seed development; flower organ identity; phase change; male sterility;
KM hybrid seed production; herbage quality; early maturing crop;
KM biomass increase; branching increase; blocking flowering;
KM allergenic pollen; floral meristem identity protein; gene; ss.
XX
XX Lolium perenne.
OS
XX WO200233091-A1.
PN
XX 25-APR-2002.
PD
XX 17-OCT-2001, 2001WO-AU001311.
PF
XX 19-OCT-2000; 2000AU-0000873.
PR
XX
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX WPI; 2002-454601/48.
XX
XX P-PSDB; ABG60945.
DR

PT New substantially purified or isolated polypeptide e.g. MADS-box,
PT CENTRORADIALIS, APTAL2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.

Claim 3; Fig 72; 290p; English.

CC The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, APTAL2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence encodes a novel floral
CC meristem identity protein involved in floral development and a potential
CC target for manipulating plant life cycles
XX
XX

SQ Sequence 1065 BP; 327 A; 254 C; 268 G; 216 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.83e-57 Length: 1065
Score: 640.00 Matches: 121
Percent Similarity: 76.06% Conservative: 41
Best Local Similarity: 56.81% Mismatches: 45
Query Match: 58.02% Indels: 6
DB: 6 Gaps: 2

US-10-069-527-2 (1-215) x ABK82127 (1-1065)

QY 1 MetGlyArgGlyValGluIleLysArgIleGluAsnSerSerAsnArgIleValThr 20
 Db 128 ATGGCGCGTGGAAAGATCGATGATCAGAGATCGAAGACCAAGCAACCCCGAGTGACC 187
 QY 21 TySerIysArgArgGlnGlyIleIleLysLysAlaLysGluIleThrValLeuCysAsp 40
 Db 188 TTCTCCAGACGCAAGAACGGATCTCAAGAGCCAGAGATCAAGCGTGGCTCTGGAC 247
 QY 41 AlalysValSerLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 60
 Db 248 GCCGAGGTCGGCGTCGCTCTCTCCAGGCGCGGAGCTCAACACTTCTCTCCCA 307
 QY 61 SerThrThrLeuThrGluIleLeuAspLysIleIleIleIleIleIleIleIleIleIleIle 80
 Db 308 AAGACATCGCTATCAAGAACTTGGAGAGTACCAACCACTCCGGGAAGATCTGTGG 367
 QY 81 AspaIalysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
 Db 368 GATAGAAACCAAGAGCTCTCAGTCGCGAGATTCGATTCGATTCAGAAAGAAATGACAAC 427
 QY 101 MetGluValGluLeuAspArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
 Db 428 ATGCAGATCGAGCTCAGGCACTTGAAGCGAAGATCTGAATCTCACTGCAACCAAGAG 487
 QY 121 LeuMetAlaLeuGluGluIleAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
 Db 488 TTGATCTGATTTGAGGAAGCACTTGATTAATGAGTGAAGGCTCGATGAAGAAACAGATG 547
 QY 141 LysAspValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
 Db 548 GAGACACACACAGACGCTGATGAAAACTGGCAAGATCTAGAAAGTGAAGCAAGTTCTC 607
 QY 161 ThrTyrGluLeuGlnLysGlnGlnGlnMetLysIleLysGluAsnValAsnMetGlu 180
 Db 608 GCATCTAAACTGCAT--CAGCAAGATATTCGCTGAACGGAAACAGAGGAGCTTGAG 664
 QY 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnIleProPhe 200
 Db 665 CTGCTTACCATCCCGACAGG-----GACTTGCAGCCCAATCCGATC 709
 QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnIle 213
 Db 710 ACGTTCCGCGTGCAGCTAGCCACCCCACTCGAGGAG 748

PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
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 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
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 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
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 PR 01-JUN-1999; 99US-0137222P.
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 PR 10-JUN-1999; 99US-0138647P.
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 PR 16-JUN-1999; 99US-0139453P.
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 PR 18-JUN-1999; 99US-0139750P.
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 PR 29-JUN-1999; 99US-0140991P.
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 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142306P.
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 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.

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Dd		643 ACITTTAGATGCAC---CAACAGCGCTGTGTCGCCGGCATGAAGAAGCTGGAG	699
Oy		181 AsmQlyTyrlhsIglnAgtgIntLeugLYAsntLyASnaAnsnnglnglninlePrope	200
Dd		700 ACCGATACCATTGAGTCCAG-----CACGACGGAGATTTCATTCCCGAGATGCCGTTC	753
Oy		201 AlapharvAlgnProlleglnProfsnleunglgu	213
Dd		754 AACTTCGGGGTGAGCCCCAACACCCCACCTGCAGAGA	792
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XX	AC	AAC35208;	
XX	DT	17-OCT-2000 (first entry)	
XX	XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 9372.	
KM	XX	Hybridisation assay; genetic mapping; gene expression control;	
KW	XX	protein identification; signal transduction pathway; metabolic pathway;	
KM	XX	promoter; termination sequence; ss.	
OS	XX	Arabidopsis thaliana.	
PN	EP	EPI033405-A2.	
XX	PD	06-SEP-2000.	
XX	Pf	25-FEB-2000; 2000EP-00301439.	
XX			
PR	25-FEB-1999;	99US-0121825P.	
PR	03-MAR-1999;	99US-0123160P.	
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PR	25-MAR-1999;	99US-0126264P.	
PR	29-MAR-1999;	99US-0126785P.	
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PR	02-JUL-1999;	99US-0142015P.	
PR	06-JUL-1999;	99US-01423	

PR	09-AUG-1999;	99US-0147493P.
PR	09-AUG-1999;	99US-0147935P.
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PR	11-AUG-1999;	99US-0148319P.
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PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
PR	01-SEP-1999;	99US-0151930P.
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PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153758P.
PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.
PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.
PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
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PR	21-OCT-1999;	99US-0160815P.
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PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
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PR	25-OCT-1999;	99US-0161406P.
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PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
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PR	29-OCT-1999;	99US-0162142P.

Best Local Similarity: 60.00%			
Query Match: 57.34%			
DB:	3	Mismatches:	40
		Indels:	14
		Gaps:	2
US-10-069-527-2 (1-215) x AAC35208 (1-909)			
QY	1	MetGlyArgGlyLysValGluIleValArgIleGluAsnSerSerAsnArgIleValThr	20
DB	84	ATGGGTAGAGAGAAAGATCGAGATTAAGAGATGAGAACCCAAACACAGAGGGGACG	143
QY	21	TyrSerLysArgArgAsnGlyIleIleLysValAlaLysGluIleThrValIleCysAsp	40
DB	144	TTCTCAAGAGAGAGATGATGCTGCAAGAGCTTAAGATTCACAGCTTGTGAT	203
QY	41	AlaLysValSerLeuIleIleTyrSerSerSerGlyLysMetValGluTyrCysSerPro	60
DB	204	GCAAAAGTTCCTCCATTAATCTTGCAGATTAAGATGATGATTAATTAATCTTCTCT	263
QY	61	SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyIleSerGlyLysLeuTyr	80
DB	264	TCATGCAATCTTGGCTGCTATGCTGACCAATACAGAGATTAATCTTGGAC	322
QY	81	AspAlaLysHisGluLeuLeuSerAsnGluValAspArgValLysLysAspAsnSer	100
DB	323	GATGCTAAGCATGAGAACTTACCAATGAGATGATGATCAAGAAAGGAAATGATAGC	382
QY	101	MetGluValGluLeuMetArgHisLeuLysGlyLysAspIleThrSerLeuAsnHisValGlu	120
DB	383	TTACAACTGAGGCTCGAGCATTTGAGAGGAGAAATATACAGCTCTCACTTGAATAAT	442
QY	121	LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer	140
DB	443	CTGATGGCTGTGCGAGCAGCGCATTTGAACATGGCTGACCAAAATCCGAGCCACGAG	502
QY	141	LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluLeuLysArgLeu	160
DB	503	GAGATCCTTATATCAAAAGAGAGAAAGAGAAATGATGCGGAGAGCAACGGCACTC	562
QY	161	ThrTyrGluLeuGluLysGlnGluMetLysIleLysGluAsnValArgAsnMetGlu	180
DB	563	ACTTCCAGCTGCA---CAACAGAGATGCTATGCAACGACCAAGAGAGAAATGAG	619
QY	181	AsnGlyTyrHisGlnArgGluLeuGlyAsnTyrAsnAsnAsnGlnGlnGlnIleProPhe	200
DB	620	ATGAGAGATCATGATGGCAG-----TTT	643
QY	201	AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle	215
DB	644	GGATATAGAGTGCACACGATTCAGCCAAATCTCAGGAAAGATT	688
RESULT 15			
AAD42258			
ID	AAD42258 standard; cDNA, 1089 BP.		
XX	AAD42258;		
DT	04-NOV-2002 (first entry)		
XX	Corn AP3 homologue cDNA from clone ctnc-pk002.j23.		
XX	Floral developmental protein; flowering locus T; APETALA3; transgenic;		
XX	FT AP3; transgenic plant; fertility; flower development; gene mapping;		
XX	tissue culture; cell division; corn; gene; ss.		
OS	Zea mays.		
XX	Key		
XX	Location/Qualifiers		
FT	120..749		
FT	/*tag= a		
FT	/product= "Corn AP3 homologue protein"		
XX	CDS		
XX	W0200244390-A2.		

Alignment Scores:
 Pred. No.: 2,87e-56
 Score: 632.50
 Percent Similarity: 75.35%

Length: 909
 Matches: 129
 Conservative: 33

XX 06-JUN-2002.
 PD 21-NOV-2001; 2001WO-US043750.
 PF 28-NOV-2000; 2000US-0253415P.
 PR (DUPLO) DU PONT DE NEMOURS & CO E. I.
 PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
 XX WPI; 2002-547703/58.
 DR P-PSDB; AAE25756.
 PT New floral developmental polypeptide having flowering locus T or Ap3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.
 PS Claim 6; Page 79; 88pp; English.

CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APERLA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or FTp1 homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is corn AP3 homologue cDNA
 CC XX

SQ Sequence 1089 BP; 295 A; 284 C; 297 G; 213 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,49e-55 Length: 1089
 Score: 623.00 Matches: 119
 Percent Similarity: 76.64% Conservative: 45
 Best Local Similarity: 55.61% Mismatches: 42
 Query Match: 56.48% Indels: 8
 DB: Gaps: 3

US-10-069-527-2 (1-215) x AAD4258 (1-1089)

QY 1 MetGlyArgGlyValGluLeuValArgIleGluAsnSerSerAsnArgInValThr 20
 Db 120 ATGGGGGCGCGCAAGATCGAGATCAAGCGATCGAGAACTCCACCAACCGCGAGTGACC 179
 QY 21 TySerIysArgArgAngIyIleIleIysValAspIleValIleThrValIleuCysAsp 40
 Db 180 TTCTCCAAAGCCCGCAACGGATCTCAAGAAGCGCGGAGATCAAGCTCTGCGAC 239
 QY 41 AlaIysValSerIleuIleIleTySerSerSerGlyIysMetValGluTyCysSerPro 60
 Db 240 GCCAGGTCGGCGTCGCTCTCTCCAGCGCCGCAAGCTTACGACTACTGCTCCCG 299
 QY 61 SerThrThrLeuThrGluIleuAspIleTyHisGlyInSerGlyIysIleuTyr 80
 Db 300 AAGACATCGCTATCAAAATCTTGAGAGAACCAACCAACTCTGAAAAGATACGTGTG 359
 QY 81 AspAlaIysHisGluAsnLeuSerAsnGluValAspArgValIysIysAspAspSer 100
 Db 360 GGTAGAAGACCAAGAGCTTATGAGAGATTGACCGTATAAAGAAAGAAAGACACAC 419
 QY 101 MetGluValGluLeuArgHisLeuIleGlyIleAspIleThrSerLeuAsnHisValGlu 120
 Db 420 ATGCAATCGAGCTCAAGCACTTAAGAGTGAAAGATCTAAACTGCTGCAACCAAGAC 479
 QY 121 LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspIysGlnSer 140

Db 480 CTGATCATGATCGAAGAGCACTTGATATGAGACTGAGCAACCTGAAATGAGAACTGATG 539
 QY 141 LysPheValAspMetMetArgAspAsnGlyIysAlaLeuGluAspGluAsnLysArgIleu 160
 Db 540 GAGCACTGGAAAGCGGTGTACAAACACTTAAGATGATGGAAGACGAGAACAAATTGCTG 599
 QY 161 ThrTyGluLeuGluIleGlnIleGlnIleMetIysIleIysGluAsnValArgAspMetGlu 180
 Db 600 GCCTCAAACTCCAC--CAGCAAGATATCCGCTGAGCGGACGACGATGAGAGCTTGAG 656
 QY 181 AsnGlyTyHis--GlnArgGluLeuGlyAsnTyAsnAsnAsnGlnGlnIlePro 199
 Db 657 CTGGATTACATCCCTGACCGGAGACTGGCG-----GCCCAAGATGCCA 698
 QY 200 PheAlaPheArgValGlnProIleGlnProAsnLeuGlnGlu 213
 Db 699 ATCACCTTCGGGTGACAGCCACCATCCCACTTGACAGAG 740

Search completed: September 26, 2004, 05:39:06
 Job time : 366.219 secs

